

## SEQUENCE LISTING

&lt;110&gt; University of Utah Research Foundation

<120> COMPOSITIONS AND METHODS FOR MODULATING  
DHR96

&lt;130&gt; 21101.0053P1

&lt;140&gt; Unassigned

&lt;141&gt; 2005-01-13

&lt;150&gt; 60/536,337

&lt;151&gt; 2004-01-13

&lt;160&gt; 60

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1543

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 1

Met	Thr	Leu	Ser	Arg	Gly	Pro	Tyr	Ser	Glu	Leu	Asp	Lys	Met	Ser	Leu	1	5	10	15
Phe	Gln	Asp	Leu	Lys	Leu	Lys	Arg	Arg	Lys	Ile	Asp	Ser	Arg	Cys	Ser	20	25	30	
Ser	Asp	Gly	Glu	Ser	Ile	Ala	Asp	Thr	Ser	Thr	Ser	Ser	Pro	Asp	Leu	35	40	45	
Leu	Ala	Pro	Met	Ser	Pro	Lys	Leu	Cys	Asp	Ser	Gly	Ser	Ala	Gly	Ala	50	55	60	
Ser	Leu	Gly	Ala	Ser	Leu	Pro	Leu	Pro	Leu	Ala	Leu	Pro	Leu	Pro	Met	65	70	75	80
Ala	Leu	Pro	Leu	Pro	Met	Ser	Leu	Pro	Leu	Pro	Leu	Thr	Ala	Ala	Ser	85	90	95	
Ser	Ala	Val	Thr	Val	Ser	Leu	Ala	Ala	Val	Val	Ala	Ala	Val	Ala	Glu	100	105	110	
Thr	Gly	Gly	Ala	Gly	Ala	Gly	Gly	Ala	Gly	Thr	Ala	Val	Thr	Ala	Ser	115	120	125	
Gly	Ala	Gly	Pro	Cys	Val	Ser	Thr	Ser	Ser	Thr	Thr	Ala	Ala	Ala	Ala	130	135	140	
Thr	Ser	Ser	Thr	Ser	Ser	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	145	150	155	160
Thr	Ser	Ser	Ser	Thr	Ser	Ser	Ala	Ser	Pro	Thr	Ala	Gly	Ala	Ser	Ser	165	170	175	
Thr	Ala	Thr	Cys	Pro	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Asn	Gly	Ser	180	185	190	
Gly	Gly	Lys	Ser	Gly	Ser	Ile	Lys	Gln	Glu	His	Thr	Glu	Ile	His	Ser	195	200	205	
Ser	Ser	Ser	Ala	Ile	Ser	Ala	Ala	Ala	Ala	Ser	Thr	Val	Met	Ser	Pro	210	215	220	
Pro	Pro	Ala	Glu	Ala	Thr	Arg	Ser	Ser	Pro	Ala	Thr	Pro	Glu	Gly	Gly	225	230	235	240

2

Cys Gly Val Arg Thr Met Val Trp Gly Tyr Glu Pro Pro Pro Pro Ser  
 725 730 735  
 Ala Gly Gln Ser His Gly Gln His Pro Gln Gln Gln Gln Gln Ser Pro  
 740 745 750  
 His His Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Gln  
 755 760 765  
 Gln Gln Gln Gln Gln Gln Gln Gln Ser Leu Gly Gln Gln Gln His  
 770 775 780  
 Cys Leu Ser Ser Pro Ser Ala Gly Ser Leu Thr Pro Ser Ser Ser Ser  
 785 790 795 800  
 Gly Gly Gly Ser Val Ser Gly Gly Gly Val Gly Gly Pro Leu Thr Pro  
 805 810 815  
 Ser Ser Val Ala Pro Gln Asn Asn Glu Glu Ala Ala Gln Leu Leu Leu  
 820 825 830  
 Ser Leu Gly Gln Thr Arg Ile Gln Asp Met Arg Ser Arg Pro His Pro  
 835 840 845  
 Phe Arg Thr Pro His Ala Leu Asn Met Glu Arg Leu Trp Ala Gly Asp  
 850 855 860  
 Tyr Ser Gln Leu Pro Pro Gly Gln Leu Gln Ala Leu Asn Leu Ser Ala  
 865 870 875 880  
 Gln Gln Gln Gln Trp Gly Ser Ser Asn Ser Thr Gly Leu Gly Gly Val  
 885 890 895  
 Gly Gly Gly Met Gly Gly Arg Asn Leu Glu Ala Pro His Glu Pro Thr  
 900 905 910  
 Asp Glu Asp Glu Gln Pro Leu Val Cys Met Ile Cys Glu Asp Lys Ala  
 915 920 925  
 Thr Gly Leu His Tyr Gly Ile Ile Thr Cys Glu Gly Cys Lys Gly Phe  
 930 935 940  
 Phe Lys Arg Thr Val Gln Asn Arg Arg Val Tyr Thr Cys Val Ala Asp  
 945 950 955 960  
 Gly Thr Cys Glu Ile Thr Lys Ala Gln Arg Asn Arg Cys Gln Tyr Cys  
 965 970 975  
 Arg Phe Lys Lys Cys Ile Glu Gln Gly Met Val Leu Gln Ala Val Arg  
 980 985 990  
 Glu Asp Arg Met Pro Gly Gly Arg Asn Ser Gly Ala Val Tyr Asn Leu  
 995 1000 1005  
 Tyr Lys Val Lys Tyr Lys Lys His Lys Lys Thr Asn Gln Lys Gln Gln  
 1010 1015 1020  
 Gln Gln Ala Ala Gln Gln Gln Gln Gln Ala Ala Ala Gln Gln Gln  
 1025 1030 1035 1040  
 His Gln Gln Gln Gln Gln His Gln Gln His Gln Gln His Gln Gln Gln  
 1045 1050 1055  
 Gln Leu His Ser Pro Leu His His His His Gln Gly His Gln Ser  
 1060 1065 1070  
 His His Ala Gln Gln Gln His His Pro Gln Leu Ser Pro His His Leu  
 1075 1080 1085  
 Leu Ser Pro Gln Gln Gln Gln Leu Ala Ala Ala Val Ala Ala Ala Ala  
 1090 1095 1100  
 Gln His Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala  
 1105 1110 1115 1120  
 Lys Leu Met Gly Gly Val Val Asp Met Lys Pro Met Phe Leu Gly Pro  
 1125 1130 1135  
 Ala Leu Lys Pro Glu Leu Leu Gln Ala Pro Pro Met His Ser Pro Ala  
 1140 1145 1150  
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Ser  
 1155 1160 1165  
 Pro His Leu Ser Leu Ser Ser Pro His Gln Gln Gln Gln Gln Gln  
 1170 1175 1180  
 Gly Gln His Gln Asn His His Gln Gln Gln Gly Gly Gly Gly Gly Gly  
 1185 1190 1195 1200

```
<210> 2
<211> 4632
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

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acgtccacct	cgtgcgcgga	cttgctggcg	cccatgtcgc	cgaagctctg	cgacagcggc		180
tggcgggggg	cgtcgctggg	ggcatcgctg	ccccctcgcg	tggccctgc	cctgccaatg		240
gccctgccac	tgcccattgc	gctgccctcg	ccccctcacg	gggcattctc	gggcgtccac		300
ctttcccttg	cacgcgctct	qccgcgcgct	qccgagacgg	gtggcgcggg	cgcggaagga		360

gctgggacag	cagtaacagc	gtcgggagca	ggaccatgcg	tctccacgtc	gtctacgacg	420
gcagcggcag	ccacatcctc	gacctcctcg	ctctcgtcct	cctcctcttc	gtcatcctcc	480
acgtcctcca	gcacttcctc	cgcctcgccg	acagctggag	cctcctccac	ggccacctgc	540
cccggccagca	gcagcagcag	cagtggaaac	ggaagtgggg	gcaaaagtgg	tagcatcaag	600
caggagcaca	cggagatata	ctcgtcgagc	agtgcgattt	cggcggccgc	cgcctcaacg	660
gtgatgtcac	cgcgcgccgc	tgaggcgacg	agatccagtc	cagccacgcc	cgagggaggg	720
ggaccagctg	gcgacgggaag	tggagcaacg	ggaggcgga	acacgagcgg	cggatcaacg	780
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agcagcgcca	agctgagcga	ggctggatg	agtgtgatac	ggtccgtgaa	ggaggagcgc	1020
ttgctcaacg	tatccagcaa	gatgtgggtg	ttccatcagc	agcgggagca	agagaccaa	1080
gcagtggcgg	ctgcagcagc	agcagcagcg	gcgggccatg	tgacggttct	agtgcgcca	1140
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agggaaaggg	aacgggaacg	cgatcgagag	agggatcgcg	aaagggaaacg	cgagcgggac	1260
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cagaagcagc	agcagcaggc	cgcacagcag	cagcagcagc	aggcggcggc	gcagcagcag	3120
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cagcagcagc	aacagcaggc	ctgcgccgat	ctctcgttta	gtcacccgca	ccagcagcag	3540
cagcagcagc	agggacagca	ccaaaaccac	caccagcaac	aaggtggggg	tggcggagga	3600
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tggacaaaaa	agttgccctt	ctacctggag	atcccggtgg	agatacatac	caaactactg	3960
acggacaagt	ggcacgagat	ccttatcctg	accacggccg	cctaccaggc	gttgcatggc	4020

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aagcggcgtg gcgagggagg aggcagcagg catggttcgc cggcgtcaac gccactgagc 4080
acgcccactg gtacgccggtt gagcacaccg ataccctcgc ccgcccagcc actgcacaag 4140
gacgaccgag agttttgtcag cgaggtgaac tcgcacctga gcacactgca aacctgcttg 4200
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ccgcagaatc cgcaggcgag gctcagtga ctgctctccc acataccaga gatccaggct 4560
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agcataaggt ag 4632

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&lt;210&gt; 3

&lt;211&gt; 803

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 3

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Met Leu Leu Glu Met Asp Gln Gln Gln Ala Thr Val Gln Phe Ile Ser
 1           5           10           15
Ser Leu Asn Ile Ser Pro Phe Ser Met Gln Leu Glu Gln Gln Gln
 20           25           30
Pro Ser Ser Pro Ala Leu Ala Ala Gly Gly Asn Ser Ser Asn Asn Ala
 35           40           45
Ala Ser Gly Ser Asn Asn Asn Ser Ala Ser Gly Asn Asn Thr Ser Ser
 50           55           60
Ser Ser Asn Asn Asn Asn Asn Asn Asn Asp Asn Asp Ala His Val
 65           70           75           80
Leu Thr Lys Phe Glu His Glu Tyr Asn Ala Tyr Thr Leu Gln Leu Ala
 85           90           95
Gly Gly Gly Gly Ser Gly Ser Gly Asn Gln Gln His His Ser Asn His
100           105           110
Ser Asn His Gly Asn His His Gln Gln Gln Gln Gln Gln Gln Gln
115           120           125
Gln Gln Gln His Gln Gln Gln Gln Gln Glu His Tyr Gln Gln Gln Gln
130           135           140
Gln Gln Asn Ile Ala Asn Asn Ala Asn Gln Phe Asn Ser Ser Ser Tyr
145           150           155           160
Ser Tyr Ile Tyr Asn Phe Asp Ser Gln Tyr Ile Phe Pro Thr Gly Tyr
165           170           175
Gln Asp Thr Thr Ser Ser His Ser Gln Gln Ser Gly Gly Gly Gly Gly
180           185           190
Gly Gly Gly Gly Asn Leu Leu Asn Gly Ser Ser Gly Gly Ser Ser Ala
195           200           205
Gly Gly Gly Tyr Met Leu Leu Pro Gln Ala Ala Ser Ser Ser Gly Asn
210           215           220
Asn Gly Asn Pro Asn Ala Gly His Met Ser Ser Gly Ser Val Gly Asn
225           230           235           240
Gly Ser Gly Gly Ala Gly Asn Gly Gly Ala Gly Gly Asn Ser Gly Pro
245           250           255
Gly Asn Pro Met Gly Gly Thr Ser Ala Thr Pro Gly His Gly Gly Glu
260           265           270
Val Ile Asp Phe Lys His Leu Phe Glu Glu Leu Cys Pro Val Cys Gly
275           280           285
Asp Lys Val Ser Gly Tyr His Tyr Gly Leu Leu Thr Cys Glu Ser Cys
290           295           300

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Lys Gly Phe Phe Lys Arg Thr Val Gln Asn Lys Lys Val Tyr Thr Cys  
 305 310 315 320  
 Val Ala Glu Arg Ser Cys His Ile Asp Lys Thr Gln Arg Lys Arg Cys  
 325 330 335  
 Pro Tyr Cys Arg Phe Gln Lys Cys Leu Glu Val Gly Met Lys Leu Glu  
 340 345 350  
 Ala Val Arg Ala Asp Arg Met Arg Gly Gly Arg Asn Lys Phe Gly Pro  
 355 360 365  
 Met Tyr Lys Arg Asp Arg Ala Arg Lys Leu Gln Val Met Arg Gln Arg  
 370 375 380  
 Gln Leu Ala Leu Gln Ala Leu Arg Asn Ser Met Gly Pro Asp Ile Lys  
 385 390 395 400  
 Pro Thr Pro Ile Ser Pro Gly Tyr Gln Gln Ala Tyr Pro Asn Met Asn  
 405 410 415  
 Ile Lys Gln Glu Ile Gln Ile Pro Gln Val Ser Ser Leu Thr Gln Ser  
 420 425 430  
 Pro Asp Ser Ser Pro Ser Pro Ile Ala Ile Ala Leu Gly Gln Val Asn  
 435 440 445  
 Ala Ser Thr Gly Gly Val Ile Ala Thr Pro Met Asn Ala Gly Thr Gly  
 450 455 460  
 Gly Ser Gly Gly Gly Gly Leu Asn Gly Pro Ser Ser Val Gly Asn Gly  
 465 470 475 480  
 Asn Ser Ser Asn Gly Ser Ser Asn Gly Asn Asn Asn Ser Ser Thr Gly  
 485 490 495  
 Asn Gly Thr Ser Gly Gly Gly Gly Gly Asn Asn Ala Gly Gly Gly Gly  
 500 505 510  
 Gly Gly Thr Asn Ser Asn Asp Gly Leu His Arg Asn Gly Gly Asn Gly  
 515 520 525  
 Asn Ser Ser Cys His Glu Ala Gly Ile Gly Ser Leu Gln Asn Thr Ala  
 530 535 540  
 Asp Ser Lys Leu Cys Phe Asp Ser Gly Thr His Pro Ser Ser Thr Ala  
 545 550 555 560  
 Asp Ala Leu Ile Glu Pro Leu Arg Val Ser Pro Met Ile Arg Glu Phe  
 565 570 575  
 Val Gln Ser Ile Asp Asp Arg Glu Trp Gln Thr Gln Leu Phe Ala Leu  
 580 585 590  
 Leu Gln Lys Gln Thr Tyr Asn Gln Val Glu Val Asp Leu Phe Glu Leu  
 595 600 605  
 Met Cys Lys Val Leu Asp Gln Asn Leu Phe Ser Gln Val Asp Trp Ala  
 610 615 620  
 Arg Asn Thr Val Phe Phe Lys Asp Leu Lys Val Asp Asp Gln Met Lys  
 625 630 635 640  
 Leu Leu Gln His Ser Trp Ser Asp Met Leu Val Leu Asp His Leu His  
 645 650 655  
 His Arg Ile His Asn Gly Leu Pro Asp Glu Thr Gln Leu Asn Asn Gly  
 660 665 670  
 Gln Val Phe Asn Leu Met Ser Leu Gly Leu Leu Gly Val Pro Gln Leu  
 675 680 685  
 Gly Asp Tyr Phe Asn Glu Leu Gln Asn Lys Leu Gln Asp Leu Lys Phe  
 690 695 700  
 Asp Met Gly Asp Tyr Val Cys Met Lys Phe Leu Ile Leu Leu Asn Pro  
 705 710 715 720  
 Ser Val Arg Gly Ile Val Asn Arg Lys Thr Val Ser Glu Gly His Asp  
 725 730 735  
 Asn Val Gln Ala Ala Leu Leu Asp Tyr Thr Leu Thr Cys Tyr Pro Ser  
 740 745 750  
 Val Asn Asp Lys Phe Arg Gly Leu Val Asn Ile Leu Pro Glu Ile His  
 755 760 765  
 Ala Met Ala Val Arg Gly Glu Asp His Leu Tyr Thr Lys His Cys Ala  
 770 775 780

Gly Ser Ala Pro Thr Gln Thr Leu Leu Met Glu Met Leu His Ala Lys  
 785 790 795 800  
 Arg Lys Gly

&lt;210&gt; 4

&lt;211&gt; 3269

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 4

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gcctccagct	cccgtctctg	ccgccgggtg	caacagcagc	aacaacgcgg	ccagcggtag	180
caacaacaac	agcgccagcg	gcaacaacac	cagcagcagc	agcaacaaca	acaacaacaa	240
taacaacgac	aatgatgcac	acgttctaac	gaaattcgag	cacgaataca	atgcctacac	300
gttgagcttg	gccggaggcg	gtgggagtg	cagcggcaat	cagcagcacc	acagcaacca	360
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tcagcagcag	cagcaagaac	actaccagca	gcaacagcaa	cagaatatcg	ccaacaatgc	480
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gcagaacaag	aaaggtctaca	cctgcgtggc	ggagcggtcg	tgccacatcg	acaagacgca	1020
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cagcagcacg	ggcaacggaa	cgtccggagg	aggaggtggc	aataatgcgg	gcggcggagg	1560
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ccacgaggct	ggaataggat	ctctgcagaa	cacggccgac	tcgaaaattgt	gcttcgattc	1680
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gctgcagaag	caaacctaca	accagggtgga	agtggatctc	ttcgagctga	tgtgcaaagt	1860
gctcgaccag	aatttggtct	cgcaagtaga	ctgggcacgg	aacaccgtct	tcttcaaggga	1920
tctgaagggtc	gacgacccaa	tgaagctgct	gcagcattcc	tggtcggaca	tgcttggtct	1980
ggatcacctg	catcatcgaa	tccataacgg	cctgcccagc	gagacgcaac	tgaacaatgg	2040
tcaggtgttc	aatctgatga	gtctgggttt	gttgggagtg	ccacagctgg	gcgattactt	2100
caacgagctg	cagaacaagc	tgcaggacct	gaaattcgat	atgggcgact	atgtctgcat	2160
gaaattccta	atcctgttga	atccaagtgt	acgggggtatt	gtcaaccgga	agaccgtctc	2220
cgagggacat	gataatgtgc	aagccgcttt	gctggactac	accctcacct	gctatccgtc	2280
agtgaatgac	aaattcagag	ggctagttaa	catcttaccg	gaaatccatg	ccatggccgt	2340
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catggaaggc	gaacgaagga	tacagcagaa	ttccgtatta	tgaatatggg	aatgcatcat	2580
cactactacc	accaactatc	acacctatac	acacacatgc	acacatttgt	tgattcaatg	2640
ttaattatta	ttacgtttac	ggttaggtct	agtttacgtt	taactaatta	attaatttgt	2700
cttaaattaa	ttcgtgtttt	atttgtagtc	cctgataaa	gaatttttaa	acacttgaa	2760



```

ctaaacgaga atatgtagta gatgtatgga tttaaattta aatacggcaa ggagaaacac 2820
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ataaattaat aaagtcgtg ttaaaaact 3269

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&lt;210&gt; 5

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 5

```

Met Tyr Thr Gln Arg Met Phe Asp Met Trp Ser Ser Val Thr Ser Lys
 1          5          10          15
Leu Glu Ala His Ala Asn Asn Leu Gly Gln Ser Asn Val Gln Ser Pro
 20          25          30
Ala Gly Gln Asn Asn Ser Ser Gly Ser Ile Lys Ala Gln Ile Glu Ile
 35          40          45
Ile Pro Cys Lys Val Cys Gly Asp Lys Ser Ser Gly Val His Tyr Gly
 50          55          60
Val Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Gln Ser
 65          70          75          80
Ser Val Val Asn Tyr Gln Cys Pro Arg Asn Lys Gln Cys Val Val Asp
 85          90          95
Arg Val Asn Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Lys Cys Leu
 100         105         110
Lys Leu Gly Met Ser Arg Asp Ala Val Lys Phe Gly Arg Met Ser Lys
 115         120         125
Lys Gln Arg Glu Lys Val Glu Asp Glu Val Arg Phe His Arg Ala Gln
 130         135         140
Met Arg Ala Gln Ser Asp Ala Ala Pro Asp Ser Ser Val Tyr Asp Thr
 145         150         155         160
Gln Thr Pro Ser Ser Ser Asp Gln Leu His His Asn Asn Tyr Asn Ser
 165         170         175
Tyr Ser Gly Gly Tyr Ser Asn Asn Glu Val Gly Tyr Gly Ser Pro Tyr
 180         185         190
Gly Tyr Ser Ala Ser Val Thr Pro Gln Gln Thr Met Gln Tyr Asp Ile
 195         200         205
Ser Ala Asp Tyr Val Asp Ser Thr Thr Tyr Glu Pro Arg Ser Thr Ile
 210         215         220
Ile Asp Pro Glu Phe Ile Ser His Ala Asp Gly Asp Ile Asn Asp Val
 225         230         235         240
Leu Ile Lys Thr Leu Ala Glu Ala His Ala Asn Thr Asn Thr Lys Leu
 245         250         255
Glu Ala Val His Asp Met Phe Arg Lys Gln Pro Asp Val Ser Arg Ile
 260         265         270
Leu Tyr Tyr Lys Asn Leu Gly Gln Glu Glu Leu Trp Leu Asp Cys Ala
 275         280         285
Glu Lys Leu Thr Gln Met Ile Gln Asn Ile Ile Glu Phe Ala Lys Leu
 290         295         300
Ile Pro Gly Phe Met Arg Leu Ser Gln Asp Asp Gln Ile Leu Leu Leu
 305         310         315         320

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<400> 6							
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acaattgcaa	ctatttcacc	aatcaaccggc	agcggcaaca	acatcagcaa	cagcacggcg		180
aaacgtttga	aacgttcacca	aagcttcgcga	tttcccacta	ataattatgt	atacgcaacg		240
tatggtttgac	atgtggagca	gcgtcacttcc	gaaactggaa	gcacacgcaa	acaatctcgg		300
tcaaagcaac	gtccaatcgc	cggcggggaca	aaacaactcc	agcggttcca	ttaaagctca		360
aattgagata	attccatgca	aagtctgcgg	cgacaagtca	tccggcggtgc	attacggagt		420
gatcacctgc	gagggctgca	agggattctt	tccaagatcg	cagagctccg	tggtcaacta		480
ccagtgtccg	cgcaacaagc	aatgtgtggt	ggaccgtggt	aatcgcaacc	gatgtcaata		540
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cagcgaccag	ctgcatcaca	acaattacaa	cagctacagc	ggcggctact	ccaacaacga		780
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cgatcccgaa	tttattagt	acgcggatgg	cgatatcaac	gatgtgctga	tcaagacgct		960
ggcggaggcg	catgccaa	caaataccaa	actggaagct	gtgcacgaca	tggtccgaaa		1020
gcagccggat	gtgtcgcgca	ttctctacta	caagaatctg	ggccaagagg	aactctggct		1080
ggactgcgcc	gagaagctta	cacaaatgat	acagaacata	atcgaaattg	ctaagctcat		1140
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caatttccgc	gatatttcca	tcttgccatc	ggaatcgctg	agcaagttca	agctgcagca		1620
ccgaatgtc	gtttttccgg	cgtcttacaa	qgaqctgttc	tcgatagatt	cgcacgaqga		1680

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gctgctcgag gactgagggc cgcaggatgt ggcaacaata attatttgag taaacactgc 1860
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tgtgatcctc gccaaaggact cacttaaaaa gaactctatc tatatacata tatatattat 1980
atatgacaga gcggatgacg caaagggaag ggaaaaatatt tcaaaaatat tgttaactca 2040
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tacgcataat taacaacttt tattgtttct aagaacttaa ctttaattaa atggaaacca 2940
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caaaactaca aaaattaaat aaattacatt ttgcaaaatt cacaaaaaat aaaacatgat 3540
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ccgaaaaaaa caacaacttt gttaaaaact gcgcataata aagaaaataa taaacaaagt 3900
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aattaaaatt tagcatatat aatgcataaa tattatgtta cgatatattac atttatataa 4140
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ca

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&lt;210&gt; 7

&lt;211&gt; 723

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 7

```

Met Ser Pro Pro Lys Asn Cys Ala Val Cys Gly Asp Lys Ala Leu Gly
 1      5      10      15
Tyr Asn Phe Asn Ala Val Thr Cys Glu Ser Cys Lys Ala Phe Phe Arg
      20      25      30
Arg Asn Ala Leu Ala Lys Lys Gln Phe Thr Cys Pro Phe Asn Gln Asn
    35      40      45

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Cys	Asp	Ile	Thr	Val	Val	Thr	Arg	Arg	Phe	Cys	Gln	Lys	Cys	Arg	Leu
50						55					60				
Arg	Lys	Cys	Leu	Asp	Ile	Gly	Met	Lys	Ser	Glu	Asn	Ile	Met	Ser	Glu
65					70					75					80
Glu	Asp	Lys	Leu	Ile	Lys	Arg	Arg	Lys	Ile	Glu	Thr	Asn	Arg	Ala	Lys
				85					90					95	
Arg	Arg	Leu	Met	Glu	Asn	Gly	Thr	Asp	Ala	Cys	Asp	Ala	Asp	Gly	Gly
			100					105					110		
Glu	Glu	Arg	Asp	His	Lys	Ala	Pro	Ala	Asp	Ser	Ser	Ser	Ser	Asn	Leu
		115					120					125			
Asp	His	Tyr	Ser	Gly	Ser	Gln	Asp	Ser	Gln	Ser	Cys	Gly	Ser	Ala	Asp
130						135					140				
Ser	Gly	Ala	Asn	Gly	Cys	Ser	Gly	Arg	Gln	Ala	Ser	Ser	Pro	Gly	Thr
145					150					155					160
Gln	Val	Asn	Pro	Leu	Gln	Met	Thr	Ala	Glu	Lys	Ile	Val	Asp	Gln	Ile
				165					170					175	
Val	Ser	Asp	Pro	Asp	Arg	Ala	Ser	Gln	Ala	Ile	Asn	Arg	Leu	Met	Arg
			180					185					190		
Thr	Gln	Lys	Glu	Ala	Ile	Ser	Val	Met	Glu	Lys	Val	Ile	Ser	Ser	Gln
	195					200						205			
Lys	Asp	Ala	Leu	Arg	Leu	Val	Ser	His	Leu	Ile	Asp	Tyr	Pro	Gly	Asp
	210					215					220				
Ala	Leu	Lys	Ile	Ile	Ser	Lys	Phe	Met	Asn	Ser	Pro	Phe	Asn	Ala	Leu
225					230					235					240
Thr	Val	Phe	Thr	Lys	Phe	Met	Ser	Ser	Pro	Thr	Asp	Gly	Val	Glu	Ile
				245					250					255	
Ile	Ser	Lys	Ile	Val	Asp	Ser	Pro	Ala	Asp	Val	Val	Glu	Phe	Met	Gln
			260					265					270		
Asn	Leu	Met	His	Ser	Pro	Glu	Asp	Ala	Ile	Asp	Ile	Met	Asn	Lys	Phe
	275						280					285			
Met	Asn	Thr	Pro	Ala	Glu	Ala	Leu	Arg	Ile	Leu	Asn	Arg	Ile	Leu	Ser
	290					295					300				
Gly	Gly	Gly	Ala	Asn	Ala	Gln	Gln	Thr	Ala	Asp	Arg	Lys	Pro	Leu	
305					310				315					320	
Leu	Asp	Lys	Glu	Pro	Ala	Val	Lys	Pro	Ala	Ala	Pro	Ala	Glu	Arg	Ala
				325					330					335	
Asp	Thr	Val	Ile	Gln	Ser	Met	Leu	Gly	Asn	Ser	Pro	Pro	Ile	Ser	Pro
			340					345					350		
His	Asp	Ala	Ala	Val	Asp	Leu	Gln	Tyr	His	Ser	Pro	Gly	Val	Gly	Glu
		355					360					365			
Gln	Pro	Ser	Thr	Ser	Ser	Ser	His	Pro	Leu	Pro	Tyr	Ile	Ala	Asn	Ser
	370					375					380				
Pro	Asp	Phe	Asp	Leu	Lys	Thr	Phe	Met	Gln	Thr	Asn	Tyr	Asn	Asp	Glu
385					390					395					400
Pro	Ser	Leu	Asp	Ser	Asp	Phe	Ser	Ile	Asn	Ser	Ile	Glu	Ser	Val	Leu
				405					410					415	
Ser	Glu	Val	Ile	Arg	Ile	Glu	Tyr	Gln	Ala	Phe	Asn	Ser	Ile	Gln	Gln
			420						425					430	
Ala	Ala	Ser	Arg	Val	Lys	Glu	Glu	Met	Ser	Tyr	Gly	Thr	Gln	Ser	Thr
		435					440						445		
Tyr	Gly	Gly	Cys	Asn	Ser	Ala	Ala	Asn	Asn	Ser	Gln	Pro	His	Leu	Gln
	450						455				460				
Gln	Pro	Ile	Cys	Ala	Pro	Ser	Thr	Gln	Gln	Leu	Asp	Arg	Glu	Leu	Asn
465					470					475					480
Glu	Ala	Glu	Gln	Met	Lys	Leu	Arg	Glu	Leu	Arg	Leu	Ala	Ser	Glu	Ala
				485					490					495	
Leu	Tyr	Asp	Pro	Val	Asp	Glu	Asp	Leu	Ser	Ala	Leu	Met	Met	Gly	Asp
			500					505					510		
Asp	Arg	Ile	Lys	Pro	Asp	Asp	Thr	Arg	His	Asn	Pro	Lys	Leu	Leu	Gln
		515					520					525			

Leu Ile Asn Leu Thr Ala Val Ala Ile Lys Arg Leu Ile Lys Met Ala  
 530 535 540  
 Lys Lys Ile Thr Ala Phe Arg Asp Met Cys Gln Glu Asp Gln Val Ala  
 545 550 555 560  
 Leu Leu Lys Gly Gly Cys Thr Glu Met Met Ile Met Arg Ser Val Met  
 565 570 575  
 Ile Tyr Asp Asp Arg Ala Ala Trp Lys Val Pro His Thr Lys Glu  
 580 585 590  
 Asn Met Gly Asn Ile Arg Thr Asp Leu Leu Lys Phe Ala Glu Gly Asn  
 595 600 605  
 Ile Tyr Glu Glu His Gln Lys Phe Ile Thr Thr Phe Asp Glu Lys Trp  
 610 615 620  
 Arg Met Asp Glu Asn Ile Leu Ile Met Cys Ala Ile Val Leu Phe  
 625 630 635 640  
 Thr Ser Ala Arg Ser Arg Val Ile His Lys Asp Val Ile Arg Leu Glu  
 645 650 655  
 Gln Asn Ser Tyr Tyr Tyr Leu Leu Arg Arg Tyr Leu Glu Ser Val Tyr  
 660 665 670  
 Ser Gly Cys Glu Ala Arg Asn Ala Phe Ile Lys Leu Ile Gln Lys Ile  
 675 680 685  
 Ser Asp Val Glu Arg Leu Asn Lys Phe Ile Ile Asn Val Tyr Leu Asn  
 690 695 700  
 Val Asn Pro Ser Gln Val Glu Pro Leu Leu Arg Glu Ile Phe Asp Leu  
 705 710 715 720  
 Lys Asn His

&lt;210&gt; 8

&lt;211&gt; 2832

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 8

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ctgtcgcgcg gacagttggt ctgatacgca gagttcctgc ctcaccacac acgaccacct      180
ccattaaaac cagccacccc ccccgagcgcc tcctccaccg acagcagctg ctccaccgca      240
ccaccaggag agggggcaatt aaaaaatcaa tcagagggcc ctaattgaaa gctgccaccg      300
tcgaaatgtc gccgcgaag aactgcgcgg tgtgcgggga caaggctctg ggctacaact      360
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agcagttcac ctgccccctt aacaaaaact gcgacatcac tgtggtcact cgacgcttct      480
gccagaaatg ccgcctgcgc aagtgcctgg atatcgggat gaagagtga aacattatgt      540
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tcattggaga cggcacggat gcgtgcgacg ccgatggcgg cgaggaaagg gatcaciaag      660
cgccggcgga tagcagcagc agcaaccttg accactactc ggggtcacag gactcgaga      720
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ttggaagcgt gggttctgtg caaaaaggaa aaaagacaaa aaaaataaac tgactttgag      2820
aaccagtggc aa

```

<210> 9

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 9

```

Met Met Lys His Pro Gln Asp Leu Ser Val Thr Asp Asp Gln Gln Leu
1          5          10          15
Met Lys Val Asn Lys Val Glu Lys Met Glu Gln Glu Leu His Asp Pro
20          25          30
Glu Ser Glu Ser His Ile Met His Ala Asp Ala Leu Ala Ser Ala Tyr
35          40          45
Pro Ala Ala Ser Gln Pro His Ser Pro Ile Gly Leu Ala Leu Ser Pro
50          55          60
Asn Gly Gly Gly Leu Gly Leu Ser Asn Ser Ser Asn Gln Ser Ser Glu
65          70          75          80
Asn Phe Ala Leu Cys Asn Gly Asn Gly Asn Ala Gly Ser Ala Gly Gly
85          90          95
Gly Ser Ala Ser Ser Gly Ser Asn Asn Asn Asn Ser Met Phe Ser Pro
100         105         110
Asn Asn Asn Leu Ser Gly Ser Gly Ser Gly Thr Asn Ser Ser Gln Gln
115         120         125
Gln Leu Gln Gln Gln Gln Gln Gln Gln Ser Pro Thr Val Cys Ala Ile
130         135         140
Cys Gly Asp Arg Ala Thr Gly Lys His Tyr Gly Ala Ser Ser Cys Asp
145         150         155         160
Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Arg Lys Asn His Gln Tyr
165         170         175
Thr Cys Arg Phe Ala Arg Asn Cys Val Val Asp Lys Asp Lys Arg Asn
180         185         190
Gln Cys Arg Tyr Cys Arg Leu Arg Lys Cys Phe Lys Ala Gly Met Lys
195         200         205

```

Lys Glu Ala Val Gln Asn Glu Arg Asp Arg Ile Ser Cys Arg Arg Thr  
 210 215 220  
 Ser Asn Asp Asp Pro Asp Pro Gly Asn Gly Leu Ser Val Ile Ser Leu  
 225 230 235 240  
 Val Lys Ala Glu Asn Glu Ser Arg Gln Ser Lys Ala Gly Ala Ala Met  
 245 250 255  
 Glu Pro Asn Ile Asn Glu Asp Leu Ser Asn Lys Gln Phe Ala Ser Ile  
 260 265 270  
 Asn Asp Val Cys Glu Ser Met Lys Gln Gln Leu Leu Thr Leu Val Glu  
 275 280 285  
 Trp Ala Lys Gln Ile Pro Ala Phe Asn Glu Leu Gln Leu Asp Asp Gln  
 290 295 300  
 Val Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu Gly Leu  
 305 310 315 320  
 Ser Arg Arg Ser Met His Leu Lys Asp Val Leu Leu Leu Ser Asn Asn  
 325 330 335  
 Cys Val Ile Thr Arg His Cys Pro Asp Pro Leu Val Ser Pro Asn Leu  
 340 345 350  
 Asp Ile Ser Arg Ile Gly Ala Arg Ile Ile Asp Glu Leu Val Thr Val  
 355 360 365  
 Met Lys Asp Val Gly Ile Asp Asp Thr Glu Phe Ala Cys Ile Lys Ala  
 370 375 380  
 Leu Val Phe Phe Asp Pro Asn Ala Lys Gly Leu Asn Glu Pro His Arg  
 385 390 395 400  
 Ile Lys Ser Leu Arg His Gln Ile Leu Asn Asn Leu Glu Asp Tyr Ile  
 405 410 415  
 Ser Asp Arg Gln Tyr Glu Ser Arg Gly Arg Phe Gly Glu Ile Leu Leu  
 420 425 430  
 Ile Leu Pro Val Leu Gln Ser Ile Thr Trp Gln Met Ile Glu Gln Ile  
 435 440 445  
 Gln Phe Ala Lys Ile Phe Gly Val Ala His Ile Asp Ser Leu Leu Gln  
 450 455 460  
 Glu Met Leu Leu Gly Gly Glu Leu Ala Asp Asn Pro Leu Pro Leu Ser  
 465 470 475 480  
 Pro Pro Asn Gln Ser Asn Asp Tyr Gln Ser Pro Thr His Thr Gly Asn  
 485 490 495  
 Met Glu Gly Gly Asn Gln Val Asn Ser Ser Leu Asp Ser Leu Ala Thr  
 500 505 510  
 Ser Gly Gly Pro Gly Ser His Ser Leu Asp Leu Glu Val Gln His Ile  
 515 520 525  
 Gln Ala Leu Ile Glu Ala Asn Ser Ala Asp Asp Ser Phe Arg Ala Tyr  
 530 535 540  
 Ala Ala Ser Thr Ala Ala Ala Ala Ala Val Ser Ser Ser Ser  
 545 550 555 560  
 Ser Ala Pro Ala Ser Val Ala Pro Ala Ser Ile Ser Pro Pro Leu Asn  
 565 570 575  
 Ser Pro Lys Ser Gln His Gln His Gln Gln His Ala Thr His Gln Gln  
 580 585 590  
 Gln Gln Glu Ser Ser Tyr Leu Asp Met Pro Val Lys His Tyr Asn Gly  
 595 600 605  
 Ser Arg Ser Gly Pro Leu Pro Thr Gln His Ser Pro Gln Arg Met His  
 610 615 620  
 Pro Tyr Gln Arg Ala Val Ala Ser Pro Val Glu Val Ser Ser Gly Gly  
 625 630 635 640  
 Gly Gly Leu Gly Leu Arg Asn Pro Ala Asp Ile Thr Leu Asn Glu Tyr  
 645 650 655  
 Asn Arg Ser Glu Gly Ser Ser Ala Glu Glu Leu Leu Arg Arg Thr Pro  
 660 665 670  
 Leu Lys Ile Arg Ala Pro Glu Met Leu Thr Ala Pro Ala Gly Tyr Gly  
 675 680 685

Thr Glu Pro Cys Arg Met Thr Leu Lys Gln Glu Pro Glu Thr Gly Tyr  
 690 695 700

<210> 10

<211> 3248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 10

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agttgaattc cagtgcggtt ggaagaaaca actgcaaaag gcaaaaacaa agacaatggt      60
tataagctgt atattccgct ttgattgata taaatgaata tatgcagtgc gccagttata      120
caactgccct gcaaaagtca ctcatataat aaaaaacgcc cgagatgaat ttcacagcgg      180
cggcaacaag tgcaataata gtaaaaaatc aaaagccaaa caacgaaatc tctcccaaaa      240
aaacgaagaa gcgtgtcgcg gtgcacaaaa gaaaaacaaa atagaaaaat acacaacaaa      300
ataatacgga gaaacgttaa ttataacgag ccacaaaatc gcataaagaa atcaacaagt      360
gtgtgtctgc ctttttttcc atattcgctt tcattcatgc ggtcaactca acaataacaa      420
ctcaaaatag caacaacaac aataacaata tcaacaagag cagcagcagt cgctgataaa      480
agccctgcag ctaaaacaac aacaaaacaa caagatagat tagaaagaac atcgtctggc      540
cattgagctt taattgccgg tcattacttc attactatgt gattggatct tcccgaccca      600
cttgtaaata aaaagtaaaa atactgggtta tgaagcatga tgaagcatcc gcaggatctg      660
agtgtcacgg atgaccagca gttaatgaag gtgaacaagg tggagaagat ggagcaggag      720
ttgcacgacc ccgaatcgga gagccacata atgcacgcgg atgccctggc ctctgcctat      780
ccggctgcct cgcagcccca cagtccgcat ggcctcgccc tcagcccca tggcgggtggg      840
ctgggactga gcaacagtag caaccagagc agcgagaact ttgcgctctg caacggaaac      900
ggaaatgcgg gcagcgcagg aggcggaagt gccagcagtg gcagcaacaa caacaacagc      960
atgtttctcac ccaacaacaa cttgagcggg agcgggaagt ggactaacag cagtcagcag      1020
caattgcagc agcaacaaca acagcaatca cgcagcggct gcgccatttg tggagatcgg      1080
gcgcagggca aacattatgg agcctccagc tgcgcagcgt gcaaaggatt cttcaggagg      1140
agtgctcagg aaaatcatca gtacacttgc agatttgcgc gaaactgcgt tgtggacaag      1200
gacaaacgga atcagtgccg ctactgccgg ctgaggaagt gcttcaaggc gggcatgaag      1260
aaggaggcgg tgcaaaacga gcgggatcgc attagctgcc gccgcacctc caatgacgac      1320
ccggatccgg gcaatgggct gtctgtgatt tccttggtta aggcggagaa tgagtcgcgt      1380
cagtcgaagg caggcgctgc catggagcca aacattaacg aggacctctc caacaagcag      1440
ttcgcgagca tcaacgatgt ctgcgagtcg atgaagcagc agctgctgac cctgggtgaa      1500
tggtgtaagc agattccggc ctttaacgag ctgcagctgg atgaccaggt ggcactgcta      1560
cgcgcccatg ctggcgagca tttgtctctc ggctgtctc gtcttctgat gcaattgaag      1620
gatgtttctc tgtgagcaa caattgtgtg atcacaaggc actgtccaga tccccttggt      1680
tcgccgaatt tggacatctc ccggatcggc gcccgatatca tcgatgaact ggtgacggtc      1740
atgaaggatg tgggtatcga tgacactgaa ttcgcttgca tcaaggccct agtcttcttc      1800
gatcccaatg ccaagggtct taatgaaccg aatcgctacg gcatcagata      1860
ctcaataatc tcgaggacta catatcagat cggcaatacg agtcgcgcgg tcgctttggc      1920
gagattctgc tcatcctgcc ggttctgcag tctattacct ggcagatgat cgagcagatc      1980
cagtttgcca agatcttttg agtgcccac attgattcat tactgcagga aatggtgttg      2040
ggaggagagt tggccgacaa tcctctgccg ctatcgccgc ccaatcagtc aaatgactac      2100
cagagtccca cccacacagg caacatggag ggcggtaatc aagttaactc ctctctggac      2160
tcgttgcca cgtccggtgg tcctggctcg catagtctgg acctggaggt gcagcacatt      2220
caggctctta tcgaggcgaa cagtgcggat gattccttcc gggcctacgc ggccagcact      2280
gcagcggcag ccgctgcagc cgtctcgtcc tcctcctctg caccgcgcat cgttgctcca      2340
gcctcgatct ctctccgct caacagcccc aagtcacaac atcaacatca gcaacatgcg      2400
acgcatacag aacaacagga gagctcctac ttggacatgc ccgtcaagca ctacaatggc      2460
agtccgtccg gaccgctgcc aacacagcac agtccccaga ggatgcattc ctaccaaaaga      2520
gcagtcgcct gcctggctga agtgtccagc gggggcgcg gattgggtct gcgcaatcct      2580
gccgatatta cgtccaacga gtacaaccgg agcggaggta gcagtgccga ggagctgctg      2640
cgacgaactc cactgaagat ccgggctccc gagatgctaa ccgcacccgc tggttatgga      2700
acggaaccct gtcgcatgac acttaaacag gagccagaga ctggttacta gaagaataac      2760
gaacggtgca atatgcagtt tgcaatagga cacccttaa gcacacaacc catacacata      2820
caggccctct cttgctgtac tccccaccaa gtgctatata gagatgaaat tgaaatgaag      2880

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aacttactta attgttatgc cttgaaccat tttgatactt tttattagtc ctaagtaggt 2940
atTTTTgaaa ttgttgctta atTTTtaatg tTTaAcgcag ttgcaatata tttttggagt 3000
catatTTTgc tcaagaagtt tattatatac aattatacta tatatataca ccatttagca 3060
tgtactgagt ttgttggtta tttggttatc ttatacttgt gcgtggatca caaaacattc 3120
atataaggcc atgcaatata ttgttttagg ttaggggtgt gtctagatta tgctgaaagt 3180
gtaatatata tTTaattTTa aacaaagaac tatttttata tgaatatgta taatatacaa 3240
actatttc

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&lt;210&gt; 11

&lt;211&gt; 556

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 11

```

Met Asp Glu Asp Cys Phe Pro Pro Leu Ser Gly Gly Trp Ser Ala Ser
1      5      10      15
Pro Pro Ala Pro Ser Gln Leu Gln Gln Leu His Thr Leu Gln Ser Gln
      20      25      30
Ala Gln Met Ser His Pro Asn Ser Ser Asn Asn Ser Ser Asn Asn Ala
      35      40      45
Gly Asn Ser His Asn Asn Ser Gly Gly Tyr Asn Tyr His Gly His Phe
      50      55      60
Asn Ala Ile Asn Ala Ser Ala Asn Leu Ser Pro Ser Ser Ser Ala Ser
      65      70      75      80
Ser Leu Tyr Glu Tyr Asn Gly Val Ser Ala Ala Asp Asn Phe Tyr Gly
      85      90      95
Gln Gln Gln Gln Gln Gln Gln Ser Tyr Gln Gln His Asn Tyr Asn
      100      105      110
Ser His Asn Gly Glu Arg Tyr Ser Leu Pro Thr Phe Pro Thr Ile Ser
      115      120      125
Glu Leu Ala Ala Ala Thr Ala Ala Val Glu Ala Ala Ala Ala Thr
      130      135      140
Val Ser Ser Pro Ser Val Gly Gly Pro Pro Pro Val Arg Arg Ala Ser
      145      150      155      160
Leu Pro Val Gln Arg Thr Val Ser Pro Ala Gly Ser Thr Ala Gln Ser
      165      170      175
Pro Lys Leu Ala Lys Ile Thr Leu Asn Gln Arg His Ser His Ala His
      180      185      190
Ala His Ala Leu Gln Leu Asn Ser Ala Pro Asn Ser Ala Ala Ser Ser
      195      200      205
Pro Ala Ser Ala Asp Leu Gln Ala Gly Arg Leu Leu Gln Ala Pro Ser
      210      215      220
Gln Leu Cys Ala Val Cys Gly Asp Thr Ala Ala Cys Gln His Tyr Gly
      225      230      235      240
Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Gln
      245      250      255
Lys Gly Ser Lys Tyr Val Cys Leu Ala Asp Lys Asn Cys Pro Val Asp
      260      265      270
Lys Arg Arg Arg Asn Arg Cys Gln Phe Cys Arg Phe Gln Lys Cys Leu
      275      280      285
Val Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser Leu Lys Gly
      290      295      300
Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Gln Glu Ser Pro
      305      310      315      320
Pro Ser Pro Pro Ile Ser Leu Ile Thr Ala Leu Val Arg Ser His Val
      325      330      335

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Asp Thr Thr Pro Asp Pro Ser Cys Leu Asp Tyr Ser His Tyr Glu Glu
      340      345      350
Gln Ser Met Ser Glu Ala Asp Lys Val Gln Gln Phe Tyr Gln Leu Leu
      355      360      365
Thr Ser Ser Val Asp Val Ile Lys Gln Phe Ala Glu Lys Ile Pro Gly
      370      375      380
Tyr Phe Asp Leu Leu Pro Glu Asp Gln Glu Leu Leu Phe Gln Ser Ala
385      390      395      400
Ser Leu Glu Leu Phe Val Leu Arg Leu Ala Tyr Arg Ala Arg Ile Asp
      405      410      415
Asp Thr Lys Leu Ile Phe Cys Asn Gly Thr Val Leu His Arg Thr Gln
      420      425      430
Cys Leu Arg Ser Phe Gly Glu Trp Leu Asn Asp Ile Met Glu Phe Ser
      435      440      445
Arg Ser Leu His Asn Leu Glu Ile Asp Ile Ser Ala Phe Ala Cys Leu
      450      455      460
Cys Ala Leu Thr Leu Ile Thr Glu Arg His Gly Leu Arg Glu Pro Lys
465      470      475      480
Lys Val Glu Gln Leu Gln Met Lys Ile Ile Gly Ser Leu Arg Asp His
      485      490      495
Val Thr Tyr Asn Ala Glu Ala Gln Lys Lys Gln His Tyr Phe Ser Arg
      500      505      510
Leu Leu Gly Lys Leu Pro Glu Leu Arg Ser Leu Ser Val Gln Gly Leu
      515      520      525
Gln Arg Ile Phe Tyr Leu Lys Leu Glu Asp Leu Val Pro Ala Pro Ala
      530      535      540
Leu Ile Glu Asn Met Phe Val Thr Thr Leu Pro Phe
545      550      555

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&lt;210&gt; 12

&lt;211&gt; 5181

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 12

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ctcgccatt ggaggcccc tgcctgtgg cagcagcttg cccagcttcc aggagaccta      60
ctccttgaag tacaacagca gcagcggtag cagccccag caggcgtcct cctcctccac      120
cgccgcccc acgcccactg accaggtgct gacctcaag atggacgagg actgcttccc      180
gcctctgtcc ggcggtgga gtgccagtc gcccgcccc tccagctcc agcagctgca      240
caccctgcag tctcaggccc agatgtcgca tcccaacagc agcaacaaca gcagcaacaa      300
cgcgggcaac agccacaaca acagtggggg ctacaactac cagggccact tcaatgccat      360
caatgccagc gccaatctgt cgcccagctc ctggccagct tccctctacg aatataatgg      420
tgtttccgca gcggacaact tctacggaca acagcagcag cagcaacagc aaagctatca      480
gcaacataac tacaactcgc acaatggcga gcgttactcg ctgccacagt ttcccacgat      540
ttcggagctg gctgcggcga ctgctgctgt cgaagctgcg gcggcgcca cagtctcctc      600
cccttcggtg ggcggtccgc cgccagtag cagagcatcg ctgccggttc agcgaaccgt      660
ttcgccagcc ggctccacgg cgcagagccc caagctggcc aagatcacac tgaaccagcg      720
gcactcccat gccatgccc atgccctaca gctcaactcg gcaccaatt cggcggaag      780
ttcgccagcg agtgccggtc tgcaggcggg ccggttgcct cagggtccgt cgcagctgtg      840
tgccgtttgt ggcgacaccg ccgctgcca gcattatgga gtgcgaacct gcgagggatg      900
caagggattc ttcaagcgga ccgtgcagaa gggctccaag tatgtctgcc tagcggaaca      960
gaattgcccg gtggacaaga ggcgcgcaa ccgttgccag ttctgccggt tccagaagtg      1020
cctggtcgta ggcattggtc aggaagtggg gcgcacggac tcgttgagg gtcgcccggg      1080
gagactgccc tcaaaaccga aatcgcccca ggagtcgcca ccatcaccac ccatctcgtt      1140
gatcacggcc ctggttcgca gccatgtcga cagactccg gatccctcgt gcctggacta      1200
cagccactat gaggagcagt cgatgagcga ggcagataag gtgcaacagt ttaccagct      1260
gctgaccagc tccgtggacg tgatcaagca gttcgccgag aagattcccc gctacttcga      1320

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tctcctgccg	gaggatcagg	agctgctctt	ccagagcgca	tcgctggaac	tgttcgctct	1380
gcggctggcc	tatcgcgcca	ggatcgatga	caccaagctg	atcttctgca	acggcacggg	1440
gtccaccgcg	acccagtgcc	tgcgctcctt	cggcgagtg	ctcaacgaca	tcatggaggt	1500
cagccgcagc	ctgcacaacc	tggagatcga	catctccgcc	ttcgctgcc	tctgtgcect	1560
aacctgatc	acagaacgcc	atggcctgcg	ggagccgaag	aaggtggagc	agctccagat	1620
gaagatcatt	ggcagtctgc	gcgaccacgt	cacctacaat	gccgaggccc	agaagaagca	1680
gcactacttc	agccgcctgc	tgggcaagct	gccggagctg	aggtccctga	gtgtccagg	1740
actgcagagg	atcttctacc	tgaagctgga	ggacctgggt	cccgcgccag	ctctcatcga	1800
gaacatgttc	gtcaccacat	tgccttctta	gaggcgatca	tcaagcgtat	catcacaact	1860
tgcttcctta	aactagcccc	taagttatgc	ctcctaggat	atacagagaa	aggaccccat	1920
aggacggacg	caactagctt	tagtagaacc	ctgaaataaa	taaactctac	aacagcaaaa	1980
acaaaaccga	accgaacaga	aatgaagcga	atagcagacc	caggccatat	ctttagtgtg	2040
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gccggggcacg	caatggcaac	actttctatc	cccggacttc	gaagcctgct	caacattcgg	2280
cactacggac	ggacaaacaa	cggacagaaa	cagaactcac	tcttgctctc	ttgccttttg	2340
ctaacttcta	gtcaattgat	ttaggcgaat	caaataaata	aataaaataa	ataagggcgt	2400
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aaaagctcga	agatagatga	gaactgtgtg	gaaatccact	atcatatcat	atagttgcta	2580
taagccgtgc	ttgccctaag	ctaagttaga	cccgcataaa	gttgatagcc	caaccaagta	2640
tttcggttat	ttcctagact	aaggctctaa	tagttatagg	ctaagactat	tctgttcgat	2700
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ctgacacaga	gagagttgca	cacaagcaca	caaactagcc	gataagttac	taaatacgat	2820
ctaatatcta	atataataaa	tataatataa	tatatataag	tccaagtatt	cggaaatcca	2880
agaacccttg	cataaccgca	gttcgtacgt	tccaaacgag	aaaagaactt	tatttaatcc	2940
tagaccactc	catctaagtt	ctcaaagaat	cgtatgtgga	tcgttggatc	tgtctctcta	3000
tatatgtgtg	tgtgttatct	cgatagaaaa	cccctctatg	tgattttgtg	atagattggc	3060
attgaactct	atataatatg	atataatata	ctataatata	tatacacgca	taaatatata	3120
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aaaacgaaac	aaaagaaaat	aaaacaaaac	agaagagtaa	acgtgaaatt	tttcgatgaa	4440
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tatacaacaa	attgaaaagc	aacagaagaa	attggcacaa	attaaattta	tatagcataa	4620
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gctatttccc	actacacccc	caaccacaca	atagataacc	taagctatgt	atgtacatta	4740
gctatgtata	tccagcccac	ttatgcgcct	actactagaa	atgcagaaag	cagaaagaga	4800
ggtgaaacct	atagacgcta	tcacaaatgt	ctatctgata	gacatcggta	ctaccaatgc	4860
tatattgcca	ggtgtgtaat	tactctttaa	ttgatctgtt	catttaccag	ttaagaacct	4920
aaatcatata	agtgttatga	tggaagaact	ataacttgca	attcaattaa	ctctgcaata	4980

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cgataacaag caaagcgaat catttcattt cgatttaatc ttttaattata tataacttaaa 5040
cgatgtaagc ccaaaacaaa cgttttttct atatctgtct tttgagcaaa ttagttatac 5100
gcaaaaccaa accgtattta cataaatgta tacaaaacaa atcgtatatt ttcattgggt 5160
tgaaataaat acataaaaaca a 5181

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<210> 13  
 <211> 278  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 13

Met	Ser	Asn	Phe	Ser	Ala	Cys	Ala	Val	Cys	Gly	Asp	Gln	Ser	Ser	Gly
1				5					10				15		
Lys	His	Tyr	Gly	Val	Ser	Cys	Cys	Asp	Gly	Cys	Ser	Cys	Phe	Phe	Lys
			20					25					30		
Arg	Ser	Val	Arg	Arg	Gly	Ser	Ser	Tyr	Ala	Cys	Ile	Ala	Leu	Val	Gly
			35				40					45			
Asn	Cys	Val	Val	Asp	Lys	Ala	Arg	Arg	Asn	Trp	Cys	Pro	Ser	Cys	Arg
	50					55				60					
Phe	Gln	Arg	Cys	Leu	Ala	Val	Gly	Met	Asn	Ala	Ala	Ala	Val	Gln	Glu
65					70				75						80
Glu	Arg	Gly	Pro	Arg	Asn	Gln	Gln	Val	Ala	Leu	Tyr	Arg	Thr	Gly	Arg
				85				90					95		
Arg	Gln	Ala	Pro	Pro	Ser	Gln	Ala	Ala	Pro	Ser	Pro	Thr	Pro	His	Ser
			100					105					110		
Gln	Ala	Leu	His	Phe	Gln	Ile	Leu	Ala	Gln	Ile	Leu	Val	Thr	Cys	Leu
		115					120					125			
Arg	Gln	Ala	Lys	Ala	Asn	Glu	Gln	Phe	Ala	Leu	Leu	Asp	Arg	Cys	Gln
		130				135					140				
Gln	Asp	Ala	Ile	Phe	Gln	Val	Val	Trp	Ser	Glu	Ile	Phe	Val	Leu	Arg
145				150					155						160
Ala	Ser	His	Trp	Ser	Leu	Asp	Ile	Ser	Ala	Met	Ile	Asp	Gly	Cys	Gly
				165				170					175		
Asp	Glu	Gln	Leu	Lys	Arg	Leu	Ile	Cys	Glu	Ala	His	Gln	Leu	Arg	Ala
			180					185				190			
Asp	Val	Leu	Glu	Leu	Asn	Phe	Met	Glu	Ser	Leu	Ile	Leu	Cys	Arg	Lys
		195				200						205			
Glu	Leu	Ala	Ile	Asn	Ala	Glu	Tyr	Ala	Val	Ile	Leu	Gly	Ser	His	Ser
		210				215					220				
Lys	Ala	Ala	Leu	Ile	Ser	Leu	Ala	Arg	Tyr	Thr	Leu	Gln	Gln	Ser	Asn
225					230					235					240
Tyr	Leu	Arg	Phe	Gly	Gln	Leu	Leu	Leu	Gly	Leu	Arg	Gln	Leu	Cys	Leu
				245					250				255		
Arg	Arg	Phe	Asp	Cys	Ala	Leu	Ser	Cys	Met	Phe	Arg	Ser	Val	Val	Arg
			260					265					270		
Asp	Ile	Leu	Lys	Thr	Leu										
			275												

<210> 14  
 <211> 837  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =

## synthetic construct

```

<400> 14
atgtcgaact tcagtgcctg cgcagtgtgc ggcgatcaga gctccgggaa gcactacggc      60
gtgtcctgct gcgatgggtg ctccctgcttt ttcaagcgga gcgtgcgggc cgggagcagc      120
tacgcctgca tcgctctggt cgggaactgt gtgggtggaca aggcgcggcg gaactggtgt      180
ccctccctgcc gcttcacagc atgcctggcc gtgggaatga acgctgctgc gggtcaggag      240
gagcgcggtc cgcgcaacca gcaggtggct ctctaccgca ctggccggag acaagctccg      300
ccatctcagg cggcgccatc cccgacgccc cactcccagg cgctgcactt ccagatcctc      360
gccagatcc ttgtcacgtg cctgcgccag gcgaaggcca acgagcagtt cgctctgttg      420
gatcgctgcc aacaagacgc catctttcag gtggtgtgga gcgagatctt cgtcctgcga      480
gcgtcccact ggtctctgga catcagcgcc atgatcgacg gctgcggcga tgagcagctc      540
aaacggctca tttgcgaggc ccaccagcta agggccgacg tcttggaact caactttatg      600
gagtccttaa tcctgtgcag aaaagaattg gccatcaatg cggagtatgc cgttatcctg      660
ggaagccact ctaaagccgc cctgatctcc ttagcccgtc acaccctgca gcaatccaac      720
tacctgcggt tcggacaact gtccttggt ctgaggcagc tgtgcctgag gcgcttcgac      780
tgcgcgcttt cttgtatggt tcgcagcggt gtcagggaca tottaaaaac actttag      837

```

<210> 15

<211> 281

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 15

```

Met Gly Met Arg Arg Glu Ala Val Gln Arg Gly Arg Val Pro Pro Thr
1      5      10      15
Gln Pro Gly Leu Ala Gly Met His Gly Gln Tyr Gln Ile Ala Asn Gly
20     25     30
Asp Pro Met Gly Ile Ala Gly Phe Asn Gly His Ser Tyr Leu Ser Ser
35     40     45
Tyr Ile Ser Leu Leu Leu Arg Ala Glu Pro Tyr Pro Thr Ser Arg Tyr
50     55     60
Gly Gln Cys Met Gln Pro Asn Asn Ile Met Gly Ile Asp Asn Ile Cys
65     70     75     80
Glu Leu Ala Ala Arg Leu Leu Phe Ser Ala Val Glu Trp Ala Lys Asn
85     90     95
Ile Pro Phe Phe Pro Glu Leu Gln Val Thr Asp Gln Val Ala Leu Leu
100    105    110
Arg Leu Val Trp Ser Glu Leu Phe Val Leu Asn Ala Ser Gln Cys Ser
115    120    125
Met Pro Leu His Val Ala Pro Leu Leu Ala Ala Ala Gly Leu His Ala
130    135    140
Ser Pro Met Ala Ala Asp Arg Val Val Ala Phe Met Asp His Ile Arg
145    150    155    160
Ile Phe Gln Glu Gln Val Glu Lys Leu Lys Ala Leu His Val Asp Ser
165    170    175
Ala Glu Tyr Ser Cys Leu Lys Ala Ile Val Leu Phe Thr Thr Asp Ala
180    185    190
Cys Gly Leu Ser Asp Val Thr His Ile Glu Ser Leu Gln Glu Lys Ser
195    200    205
Gln Cys Ala Leu Glu Glu Tyr Cys Arg Thr Gln Tyr Pro Asn Gln Pro
210    215    220
Thr Arg Phe Gly Lys Leu Leu Leu Arg Leu Pro Ser Leu Arg Thr Val
225    230    235    240
Ser Ser Gln Val Ile Glu Gln Leu Phe Phe Val Arg Leu Val Gly Lys
245    250    255

```

Thr Pro Ile Glu Thr Leu Ile Arg Asp Met Leu Leu Ser Gly Asn Ser  
 260 265 270  
 Phe Ser Trp Pro Tyr Leu Pro Ser Met  
 275 280

<210> 16  
 <211> 2866  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 16

ctaaattggt	gttttcaaaa	gaaatgaatt	tctttccact	cctttcagaa	ttcaagaata	60
aatattgaag	caatatggct	tcccttggtc	aaaccgatca	atcgttgcaa	atctttcttc	120
aagcgctcgg	tgcgacgtaa	tctaacttac	tcttgccgcg	gcagcagaaa	ctgtcccata	180
gatcaacacc	atcgcaatca	atgtcaatat	tgtcgattga	agaagtgcct	caaaatgggc	240
atgagacgcg	aagctgttca	acgtggacgc	gtaccaccca	ctcagcccgg	tctggccggc	300
atgcatgggc	agtaccagat	tgccaacggg	gatcccatgg	gcattgccgg	ctttaacggg	360
cactcgtacc	tcagttccta	catctcgctc	ctgctgcggg	cggaaccgta	tccgacttcg	420
cgatatggcc	agtgcagtc	acccaacaac	attatgggca	tcgacaacat	ctgcgaactg	480
gccgcccgc	tgctcttctc	ggcggtcgag	tgggccaaga	acataccctt	cttcccggag	540
ctgcaggtga	ccgaccaggt	ggccctgctc	cggctcgtct	ggtcagagct	cttcgtccta	600
aacgccagcc	agtgtcccat	gccgctccat	gtggcgccac	tgctggccgc	cgcgggactt	660
catgcctccc	cgatggccgc	cgatcgtgtg	gtggccttca	tggaccacat	ccgcattctc	720
caggagcagg	tggagaagct	gaaggcgctg	catgtcgact	ccgcggagta	ctcctgcctc	780
aaggcgatcg	tgctcttcc	caccgatgcc	tgcggcctgt	ccgatgtgac	gcacattgaa	840
tccctgcaag	agaagtgcga	gtgcgccctc	gaggaatact	gccggaccga	gtatcccaac	900
cagcccacga	gattcggcaa	gtgcttctc	agactgccat	cgctgcgaac	gggtctccta	960
caagtcattg	agcaattggt	ttttgtgcgt	ctagtcggaa	aaacgccaat	tgaaacgctg	1020
atacgcgata	tgctgctgag	cggcaacagt	ttctcctggc	cctatctgcc	ttcgatgtga	1080
cacacgatgt	ggcgccaatt	gacaacaact	tgatcatcgg	ccgcagctgt	ggcggctgca	1140
acgctcaaca	tcaattccgg	cggaggcggc	atcggcatcg	gcggcggggg	cagtggcagt	1200
ggcggtggcg	gtagtggagg	cgggtggcga	gtcgttggat	gtggcagcca	caacgttgct	1260
gctgccagtc	atgaccagct	cgccaatggt	gctgtcatgc	agcaaacata	cggcagcggc	1320
ggcagcagca	gcagcagcat	cagcggttgc	cacaacggta	acaacggcag	cggcggcagc	1380
atttgcaatc	agcagatcaa	caactacggc	aacaacagca	acaacaatgt	cggcaatcat	1440
atgagtgcag	gcagtttttt	cgggtgggtcc	aacaacagca	tccacagtag	tggaatagc	1500
aataccgatt	atatgaccac	gccagccacc	gcttatgcga	caccagcgac	agcagccaca	1560
tccacggtga	acaccacaac	gatgctgtct	aattactgcy	atgccgccac	catgatgatg	1620
gccgctgctg	aatcaatgc	aatcaatgc	ctgcagcaac	atcaccagcg	catggtgctc	1680
gcgggcagca	gcaacagcag	cagcaacaac	agcagcagca	acagcaacgg	cgcagcagca	1740
atgcccctct	catcctcgtc	tggctcactg	tcatctgcct	catcgacccc	aacagcaaca	1800
gcaactgcga	ctgcaattgc	aacagcaaca	gcaactgcag	cagcaacagc	cgcgcagcaa	1860
caacagcaac	aatcgccgcc	aaatttaatc	gatatcagcg	aagttcctct	cattgtggat	1920
gtcaagtagt	gtaattatct	atgcattctag	aaatggggct	ataaaccaac	cttgtagata	1980
ccccgccccg	ccccaccac	taccacaaaa	accataaaaac	ccccaaaaaa	aaacaattga	2040
aaaatgtaaa	aaaaaaaaag	tggaggatga	gcgcgcgcta	gcttaattga	ctaattttcc	2100
atttgtagct	tttggtgtaa	ctttgtacat	aactcctcga	aaaattcaag	ttttctctta	2160
ggccacccca	gctgtgagca	aaaccaatct	cagctgacat	atccaagaga	acttcaaaaag	2220
tgaagccccc	aaaaaaaagta	agaaggcgcc	aaaaaaacgt	ctttacatat	gaatgtgtat	2280
aatatttaaa	tggcactgag	ttctacttaa	tttttagacca	caaacacttg	aaaaaatcaa	2340
tgaaaaaata	agaattgtgg	aaagagaaaa	atccccctta	acactttcaa	aagacaaaac	2400
ataaagatag	ttaaaatatt	tatatatgta	atgtagcata	tacacgtata	tagtacatat	2460
atgaatatat	aaacgaaaact	ctactcccag	tggtttgcag	aaatatacca	aaaattttta	2520
gctatgttta	cttgatgtgt	ggcaattttt	atgtgtgctt	tagcaatttt	atttttactt	2580
taagtaaaat	ttaaaattta	taaacattcg	attctcgact	ggtttttctc	ggcggatgta	2640
tctcaaagat	gcttctgtat	gggaaggccg	aattgttgaa	atacgaatgc	aaaatttagc	2700

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gaatttttta ttttagtaacc attacgagta aaaacacaaa atgttcagtg caagtttcag 2760
ttcttaaacy attttttcgt aagcttaagc attatcttat ttatgtgtat agagtatgaa 2820
aagttttcta tattttgtaa taataaaaaat ttgcgtttat aatgaa 2866

```

&lt;210&gt; 17

&lt;211&gt; 452

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 17

```

Met Gln Ser Ser Glu Gly Ser Pro Asp Met Met Asp Gln Lys Tyr Asn
 1          5          10          15
Ser Val Arg Leu Ser Pro Ala Ala Ser Ser Arg Ile Leu Tyr His Val
 20          25          30
Pro Cys Lys Val Cys Arg Asp His Ser Ser Gly Lys His Tyr Gly Ile
 35          40          45
Tyr Ala Cys Asp Gly Cys Ala Gly Phe Phe Lys Arg Ser Ile Arg Arg
 50          55          60
Ser Arg Gln Tyr Val Cys Lys Ser Gln Lys Gln Gly Leu Cys Val Val
 65          70          75          80
Asp Lys Thr His Arg Asn Gln Cys Arg Ala Cys Arg Leu Arg Lys Cys
 85          90          95
Phe Glu Val Gly Met Asn Lys Asp Ala Val Gln His Glu Arg Gly Pro
100          105          110
Arg Asn Ser Thr Leu Arg Arg His Met Ala Met Tyr Lys Asp Ala Met
115          120          125
Met Gly Ala Gly Glu Met Pro Gln Ile Pro Ala Glu Ile Leu Met Asn
130          135          140
Thr Ala Ala Leu Thr Gly Phe Pro Gly Val Pro Met Pro Met Pro Gly
145          150          155          160
Leu Pro Gln Arg Ala Gly His His Pro Ala His Met Ala Ala Phe Gln
165          170          175
Pro Pro Pro Ser Ala Ala Ala Val Leu Asp Leu Ser Val Pro Arg Val
180          185          190
Pro His His Pro Val His Gln Gly His His Gly Phe Phe Ser Pro Thr
195          200          205
Ala Ala Tyr Met Asn Ala Leu Ala Thr Arg Ala Leu Pro Pro Thr Pro
210          215          220
Pro Leu Met Ala Ala Glu His Ile Lys Glu Thr Ala Ala Glu His Leu
225          230          235          240
Phe Lys Asn Val Asn Trp Ile Lys Ser Val Arg Ala Phe Thr Glu Leu
245          250          255
Pro Met Pro Asp Gln Leu Leu Leu Leu Glu Glu Ser Trp Lys Glu Phe
260          265          270
Phe Ile Leu Ala Met Ala Gln Tyr Leu Met Pro Met Asn Phe Ala Gln
275          280          285
Leu Leu Phe Val Tyr Glu Ser Glu Asn Ala Asn Arg Glu Ile Met Gly
290          295          300
Met Val Thr Arg Glu Val His Ala Phe Gln Glu Val Leu Asn Gln Leu
305          310          315          320
Cys His Leu Asn Ile Asp Ser Thr Glu Tyr Glu Cys Leu Arg Ala Ile
325          330          335
Ser Leu Phe Arg Lys Ser Pro Pro Ser Ala Ser Ser Thr Glu Asp Leu
340          345          350
Ala Asn Ser Ser Ile Leu Thr Gly Ser Gly Ser Pro Asn Ser Ser Ala
355          360          365

```

```

Ser Ala Glu Ser Arg Gly Leu Leu Glu Ser Gly Lys Val Ala Ala Met
   370                               375                               380
His Asn Asp Ala Arg Ser Ala Leu His Asn Tyr Ile Gln Arg Thr His
385                               390                               395                               400
Pro Ser Gln Pro Met Arg Phe Gln Thr Leu Leu Gly Val Val Gln Leu
   405                               410                               415
Met His Lys Val Ser Ser Phe Thr Ile Glu Glu Leu Phe Phe Arg Lys
   420                               425                               430
Thr Ile Gly Asp Ile Thr Ile Val Arg Leu Ile Ser Asp Met Tyr Ser
   435                               440                               445
Gln Arg Lys Ile
   450

```

&lt;210&gt; 18

&lt;211&gt; 1885

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 18

```

gagtcacacat cggagtaacc aaggatatat cgaatatatc acacaatccg caataccgcc      60
gtccacccaa accgttaaaa caaaaatcca aaacgactca aagatacacc agtgccaagt      120
gaaattcaat ttgtgcaagc gtttctacaa aaatcgccaa aattacgcc ccatcggtta      180
tgcagtcgctc ggagggttca ccagacatga tggatcagaa atacaacagc gtgcgtcttt      240
cgccagcggc atcgagtcgc attctatacc atgtgccctg caaagtctgc agagatcaca      300
gctccggcaa gcattacggc atctacgcct gtgatggctg cgccggattc ttcaagagga      360
gcattcgag atcccggcag tatgtgtgca agtcgcagaa gcagggactc tgtgtggtgg      420
acaagacgea caggaacca ttagaggctt gccgactgag gaagtgcctt gaggtcggaa      480
tgaacaagga tgcagtgcag cagagcggg gaccgcgaa ctccactctg cgtcgccaca      540
tgcccatgta caaggatgct atgatgggcg ccggcgagat gccacaaata cccgccgaaa      600
ttctgatgaa cacggctgcc ttgaccggct ttcttgagat accgatgcc atgcctggcc      660
tgccccagag ggctggtcat catcctgctc acatggctgc cttccagccg ccaccatcgg      720
ctgcccgtgt cttggactta tccgtgccac gagtgcccca tcacccggtg caccaaggac      780
accacggttt cttctcgccc accgccgcct acatgaatgc cctggccact cgggccctgc      840
ccccactcc tccgctgatg gcagctgagc acatcaagga aaccgcggcg gaacacctat      900
tcaagaacgt caactggatc aagagcgtac gggccttcac cgaactgcc atgccggatc      960
agctgctcct gctggaggag tcctggaagg agttcttcat cctggccatg gcccagtacc     1020
taatgcccat gaatttcgcc cagctgctgt tcgtctacga gtccgagaat gccaacggg     1080
agatcatggg catggtgacc cgcgaggtgc acgccttcca ggaggtgctg aaccaactgt     1140
gccatctgaa cattgacagc accgagtagc agtgtctgag ggctatttcg ctcttccgta     1200
agtcaccacc gtoggcaagt tctaccgagg atttagccaa cagctcaatc ctgacaggaa     1260
gcggcagccc gaactcctcg gcctctgctg aatccagggg tcttctggag tcgggaaaag     1320
tgggcgccat gcacaacgat gcccggagtg cgctgcacaa ctacatccag aggacccatc     1380
cctcgcagcc catgcgattc cagacgctct tgggcgtggg gcagctgatg cacaaggctc     1440
caagcttcac catcgaggag ctgttcttcc gaaagacatc cggcgacatc accattgtgc     1500
gcctcatctc cgacatgtac agtcagcgca agatctgaaa agtatgtaga gcctagacta     1560
atcgccgcac tcgaagtgcc ttccaagtgc tgggaactgt gataatctcg gaagaagcgc     1620
tttgacaat actogactcag tgaatatcaac gatttctcat atccaggagt cgagccttaa     1680
aatacgtaca caacactcac cttaataacct tacctaaaca gaactcgaag taatcttagc     1740
taaagtctct cagaccatcc agatgtgttt caaattgcat tcgcaaaagt ttcaactttg     1800
cctgttaa at acgtcaatcg tagttttaaa cacttttagt ttaagcgcat attattagct     1860
ttaggatttg gaaaaataat tatttc

```

&lt;210&gt; 19

&lt;211&gt; 691

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct.

&lt;400&gt; 19

```

Met Gly Thr Ala Gly Asp Arg Leu Leu Asp Ile Pro Cys Lys Val Cys
 1           5           10           15
Gly Asp Arg Ser Gly Lys His Tyr Gly Ile Tyr Ser Cys Asp Gly
 20           25           30
Cys Ser Gly Phe Phe Lys Arg Ser Ile His Arg Asn Arg Ile Tyr Thr
 35           40           45
Cys Lys Ala Thr Gly Asp Leu Lys Gly Arg Cys Pro Val Asp Lys Thr
 50           55           60
His Arg Asn Gln Cys Arg Ala Cys Arg Leu Ala Lys Cys Phe Gln Ser
 65           70           75           80
Ala Met Asn Lys Asp Ala Val Gln His Glu Arg Gly Pro Arg Lys Pro
 85           90           95
Lys Leu His Pro Gln Leu His His His His His His Ala Ala Ala Ala
100           105           110
Ala Ala Ala Ala His His Ala Ala Ala Ala His His His His His His
115           120           125
His His His Ala His Ala Ala Ala Ala His His Ala Ala Val Ala Ala
130           135           140
Ala Ala Ala Ser Gly Leu His His His His His Ala Met Pro Val Ser
145           150           155           160
Leu Val Thr Asn Val Ser Ala Ser Phe Asn Tyr Thr Gln His Ile Ser
165           170           175
Thr His Pro Pro Ala Pro Ala Ala Pro Pro Ser Gly Phe His Leu Thr
180           185           190
Ala Ser Gly Ala Gln Gln Gly Pro Ala Pro Pro Ala Gly His Leu His
195           200           205
His Gly Gly Ala Gly His Gln His Ala Thr Ala Phe His His Pro Gly
210           215           220
His Gly His Ala Leu Pro Ala Pro His Gly Gly Val Val Ser Asn Pro
225           230           235           240
Gly Gly Asn Ser Ser Ala Ile Ser Gly Ser Gly Pro Gly Ser Thr Leu
245           250           255
Pro Phe Pro Ser His Leu Leu His His Asn Leu Ile Ala Glu Ala Ala
260           265           270
Ser Lys Leu Pro Gly Ile Thr Ala Thr Ala Val Ala Ala Val Val Ser
275           280           285
Ser Thr Ser Thr Pro Tyr Ala Ser Ala Ala Gln Thr Ser Ser Pro Ser
290           295           300
Ser Asn Asn His Asn Tyr Ser Ser Pro Ser Pro Ser Asn Ser Ile Gln
305           310           315           320
Ser Ile Ser Ser Ile Gly Ser Arg Ser Gly Gly Gly Glu Glu Gly Leu
325           330           335
Ser Leu Gly Ser Glu Ser Pro Arg Val Asn Val Glu Thr Glu Thr Pro
340           345           350
Ser Pro Ser Asn Ser Pro Pro Leu Ser Ala Gly Ser Ile Ser Pro Ala
355           360           365
Pro Thr Leu Thr Thr Ser Ser Gly Ser Pro Gln His Arg Gln Met Ser
370           375           380
Arg His Ser Leu Ser Glu Ala Thr Thr Pro Pro Ser His Ala Ser Leu
385           390           395           400
Met Ile Cys Ala Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
405           410           415
Asn Gly Glu His Lys Gln Ser Ser Tyr Thr Ser Gly Ser Pro Thr Pro
420           425           430
Thr Thr Pro Thr Pro Pro Pro Arg Ser Gly Val Gly Ser Thr Cys
435           440           445

```

Asn Thr Ala Ser Ser Ser Ser Gly Phe Leu Glu Leu Leu Leu Ser Pro  
 450 455 460  
 Asp Lys Cys Gln Glu Leu Ile Gln Tyr Gln Val Gln His Asn Thr Leu  
 465 470 475 480  
 Leu Phe Pro Gln Gln Leu Leu Asp Ser Arg Leu Leu Ser Trp Glu Met  
 485 490 495  
 Leu Gln Glu Thr Thr Ala Arg Leu Leu Phe Met Ala Val Arg Trp Val  
 500 505 510  
 Lys Cys Leu Met Pro Phe Gln Thr Leu Ser Lys Asn Asp Gln His Leu  
 515 520 525  
 Leu Leu Gln Glu Ser Trp Lys Glu Leu Phe Leu Leu Asn Leu Ala Gln  
 530 535 540  
 Trp Thr Ile Pro Leu Asp Leu Thr Pro Ile Leu Glu Ser Pro Leu Ile  
 545 550 555 560  
 Arg Glu Arg Val Leu Gln Asp Glu Ala Thr Gln Thr Glu Met Lys Thr  
 565 570 575  
 Ile Gln Glu Ile Leu Cys Arg Phe Arg Gln Ile Thr Pro Asp Gly Ser  
 580 585 590  
 Glu Val Gly Cys Met Lys Ala Ile Ala Leu Phe Ala Pro Glu Thr Ala  
 595 600 605  
 Gly Leu Cys Asp Val Gln Pro Val Glu Met Leu Gln Asp Gln Ala Gln  
 610 615 620  
 Cys Ile Leu Ser Asp His Val Arg Leu Arg Tyr Pro Arg Gln Ala Thr  
 625 630 635 640  
 Arg Phe Gly Arg Leu Leu Leu Leu Leu Pro Ser Leu Arg Thr Ile Arg  
 645 650 655  
 Ala Ala Thr Ile Glu Ala Leu Phe Phe Lys Glu Thr Ile Gly Asn Val  
 660 665 670  
 Pro Ile Ala Arg Leu Leu Arg Asp Met Tyr Thr Met Glu Pro Ala Gln  
 675 680 685  
 Val Asp Lys  
 690

&lt;210&gt; 20

&lt;211&gt; 3043

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 20

gtcagcccag	gcatccgca	tttgcgtccg	cagcaggttt	ccgatttcag	aactctgatt	60
ccagcggcag	cgaatcgct	cggcatctga	acatttgaaa	ataatctaaa	attgcaagtg	120
actttgtgca	ccggttacac	taaaattggt	aacaaatcgc	catatattct	gaatttaa	180
ttaaagtgcg	cagtgcggaa	tataaatcag	agcaaactgg	ataggttagg	gttcaaatac	240
ttccatcaac	ggaaaatggg	cacagcgggc	gatcgccctgt	tggacattcc	ctgcaaggtg	300
tgtggcgatc	gcagctccgg	caagcactat	ggaatctaca	gctgcgatgg	ctgctccggt	360
tttttcaagc	ggagcattca	tcgcaatcgg	atttacacct	gtaaggccac	cggcgatctc	420
aagggtcgct	gtccggtgga	caagacccat	cggaatcagt	gtcgcgcctg	tcgcctggcc	480
aagtgtcttc	agtcggccat	gaacaaggat	gctgtgcagc	acgagcgcgg	tcctaggaaa	540
cccaagttgc	acccgcaact	gcatcatcat	catcatcatg	ctgctgccgc	cgccgtgca	600
gcgcatcatg	cagcagccgc	ccatcaccat	caccatcatc	accaccacgc	ccacgcagcg	660
gccgcccac	atgcggcagt	ggctgcagcg	gctgcctccg	ggctgcatca	ccaccaccac	720
gccatgcccg	tctcgctggt	gaccaatgtc	tcggcctcgt	tcaactatac	gcagcacatc	780
tccacgcac	cgcctgctcc	ggcggcgcca	cccagtggtc	ttcacctgac	ggccagtggc	840
gcccagcagg	gaccagctcc	accagctggc	cacctgcacc	atggtggagc	cggacatcag	900
cacgccacgg	ccttcaccca	tccgggacat	ggacacgcgc	tgccctgccc	acatggcgcg	960
gtcgtcagca	taccggcgcg	caactcgagc	gcaatctccg	gcagcgggtc	cggctccacg	1020
ctgcccttcc	cctcgcacct	gctgcaccac	aatctgatag	cggaggcggc	cagcaagctg	1080

```

ccgggcatca ctgccacagc cgttgcgggc gtggtgtcct ccactagcac gccctacgcc 1140
tcggcgggccc agacgtcgtc gcctagtagc aacaaccaca actactcttc gccctcgccc 1200
agcaactcca tccagtcatt ctgcagcatt ggatcgcgca gcggtggtgg cgaggagggc 1260
ctcagcctgg gcagcgagag tccgcgcgtc aatgtggaaa cggagacacc ttcgccatcg 1320
aactcgccgc cccttagtgc tggtagcatt tcgccagcgc ccacgttgac cacctcgtcg 1380
ggatcgccgc agcaccgcca gatgtcgcg cagagcctca gtgaggcaac cagcccgccc 1440
agccacgect ctctcatgat ttgcgccagc aacaataaca ataacaacaa taataataac 1500
aataatggag agcacaagca gtcgagctac acatccggat caccgacacc cacaacgccc 1560
acgcccgcac cgccgcgttc tgggtgtaggt tccacctgca acacggccag cagctccagc 1620
ggcttctctg agtgctgct cagtccggac aagtgcagg agctcatcca gtaccaggtg 1680
cagcacaaca cgctgctctt cccgcaacag ctggttggaet cgcggtgct ctctggggag 1740
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atgcccttcc agacgtctct caagaacgac cagcatttgc tgctccagga atcctggaag 1860
gagctcttcc tgctcaacct cgcccaatgg actataccgc tggatctaac gcccatactg 1920
gaatcaccgc tcattccgca acgggtgctg caggacgagg ccacacaaac ggagatgaag 1980
acgatccagg agatcctctg ccgcttccgc cagatcacac ccgacggcag cgaggtgggc 2040
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gtggagatgt tgcaggatca ggcgcagtgc atcctctccg accatgtgcg actgcgctac 2160
cctcgccaag caaccgcgtt cggcaggctg ctgctcctgc tgccctcgct gcgcaccatc 2220
cggcgggcca ccattcgagg gctgttcttc aaggagacca tcggcaatgt gccattgct 2280
cgactgctgc gcgacatgta caccatggaa ccggcacagg tggacaagtg aaccggccac 2340
gcatgacagt cgaatgaaa tcaaatcga ttccttagca cctaagcgcc acccatcggt 2400
cgctcgcata tgcgaactta tttgtattcc aatgcgaccc gaatcctatt cagattcact 2460
gcggcaggag gcggtccaaa tgtggggcgg aagctgcaga tgctatggtt cgcaggacgc 2520
catgtaatgg aggcgtatgt actaaccgcg ctctctcatt ggcatgcag tccgcgatga 2580
tggcgacatc ccacaccac acccgatccc acacctgat ttatcgccgg caatgcgtcg 2640
gagtctcctt actttcgctt cgttttctaa catttgatc cttattttat ttcattcttt 2700
tccacggatt tttcgtttg actgcctggg cggcactctt tatttatctt tcattcgacg 2760
ttttgtcgtc gcttttctaa aaattcccca tgttatttca acctggcaag gacctcgag 2820
tccattcccc gcgcccttac ttacaaatca cttcccatcc cacatccagc aattccgtgg 2880
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agttgtaatt ctttttctg caatccagct ctaaacggg tttcttaatc gaaatcgata 3000
aatgtaaaaa ttatacatat cctttaccaa cattgtttgc cta 3043

```

&lt;210&gt; 21

&lt;211&gt; 532

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 21

```

Met Ala Thr Gly Arg Ser Leu Leu Phe Arg Val Pro Trp Tyr Val Cys
 1           5           10           15
Leu Cys Val Cys Ala Glu Ser Ala Glu Pro Gly Val Tyr Trp Arg Leu
 20           25           30
Arg Leu Arg Leu Gly Leu Pro Thr Leu Ala Gly Pro His Thr Asn Thr
 35           40           45
Leu Thr Leu Thr Ala Arg Thr Ser Ser Cys Arg Ser Ile Lys Lys Glu
 50           55           60
Arg Ile Lys Ala Ser Gln Gln Ala Asn Ala Pro Pro Glu Leu Pro Leu
 65           70           75           80
Lys Val Ser Val Asp Val Asn Ile Ile Ile Ala Ala His Ser Gln Arg
 85           90           95
Arg Arg Ile Gly Leu Val Arg Phe His Gln Arg Glu Ser Glu Asp Arg
100          105          110
Pro Leu Ala Val Ala Ser Pro Arg Leu Gln Ile Asn Met Glu Pro Thr
115          120          125

```

Ala Met Asn Pro Lys Lys Leu His Ser Pro Gln Arg His Cys Tyr Thr  
 130 135 140  
 Pro Pro Pro Ala Pro Met His Gly Gln Ala Pro Pro Pro Thr Ser Thr  
 145 150 155 160  
 Gly Val Ala Pro Pro Thr Gln Pro Pro Pro Pro His Pro Ala Ala Pro  
 165 170 175  
 Asn Val Pro Asn Gly Arg Leu Leu Ser Trp Asn His Ser Ala Ala Ala  
 180 185 190  
 Ala Ala Ala Ala Ala Ala Gln Ala Ala Ala Asn Ser Met Asn His  
 195 200 205  
 Ser Ser Ala Ala Glu Gly Ser Ser Met Thr Arg Ile Lys Gly Gln Asn  
 210 215 220  
 Leu Gly Leu Ile Cys Val Val Cys Gly Asp Thr Ser Ser Gly Lys His  
 225 230 235 240  
 Tyr Gly Ile Leu Ala Cys Asn Gly Cys Ser Gly Phe Phe Lys Arg Ser  
 245 250 255  
 Val Arg Arg Lys Leu Ile Tyr Arg Cys Gln Ala Gly Thr Gly Arg Cys  
 260 265 270  
 Val Val Asp Lys Ala His Arg Asn Gln Cys Gln Ala Cys Arg Leu Lys  
 275 280 285  
 Lys Cys Leu Gln Met Gly Met Asn Lys Asp Asp Asp Ser Ile Asp Val  
 290 295 300  
 Thr Asn Asp Asn Glu Glu Pro His Ala Val Ser Arg Ser Asp Ser Ser  
 305 310 315 320  
 Phe Ile Met Pro Gln Phe Met Ser Pro Asn Leu Tyr Thr His Gln His  
 325 330 335  
 Glu Thr Val Tyr Glu Thr Ser Ala Arg Leu Leu Phe Met Ala Val Lys  
 340 345 350  
 Trp Ala Lys Asn Leu Pro Ser Phe Ala Arg Leu Ser Phe Arg Asp Gln  
 355 360 365  
 Val Ile Leu Leu Glu Glu Ser Trp Ser Glu Leu Phe Leu Leu Asn Ala  
 370 375 380  
 Ile Gln Trp Cys Ile Pro Leu Asp Pro Thr Gly Cys Ala Leu Phe Ser  
 385 390 395 400  
 Val Ala Glu His Cys Asn Asn Leu Glu Asn Asn Ala Asn Gly Asp Thr  
 405 410 415  
 Cys Ile Thr Lys Glu Glu Leu Ala Ala Asp Val Arg Thr Leu His Glu  
 420 425 430  
 Ile Phe Cys Lys Tyr Lys Ala Val Leu Val Asp Pro Ala Glu Phe Ala  
 435 440 445  
 Cys Leu Lys Ala Ile Val Leu Phe Arg Pro Glu Thr Arg Gly Leu Lys  
 450 455 460  
 Asp Pro Ala Gln Ile Glu Asn Leu Gln Asp Gln Ala His His Thr Lys  
 465 470 475 480  
 Thr Gln Phe Thr Ala Gln Ile Ala Arg Phe Gly Arg Leu Leu Leu Met  
 485 490 495  
 Leu Pro Leu Leu Arg Met Ile Ser Ser His Lys Ile Glu Ser Ile Tyr  
 500 505 510  
 Phe Gln Arg Thr Ile Gly Asn Thr Pro Met Glu Lys Val Leu Cys Asp  
 515 520 525  
 Met Tyr Lys Asn  
 530

&lt;210&gt; 22

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 22

```

atggcgaccg ggcgttctct gctctttcga gtgccttggt atgtgtgctt gtgtgtgtgc 60
gcagagagcg cagagccggg tgtttattgg agattgcgat tgcggcttgg cttaccacaca 120
ctcgcagggc cgcacaccaa cacactaaca ctaacagcga ggacaagctc ctgccgcagc 180
atcaagaagg aacgaatcaa agcaagccaa caagcaaatg cgccaccaga gttgccacta 240
aaagtctccg ttgacgttaa catcatcatc gcggcacact cgcagcgccg tcggatcgga 300
ttggttcggg ttcatcagcg ggaatcagag gaccgtccac ttgccgtcgc ctctccacga 360
ttgcaaatta atatggagcc tactgcgatg aacccgaaaa aactccacag tccgcagcgg 420
cattgtctaca ctccgcccgc ggcgcggatg cacggacagg cgcctccacc tacatcaacg 480
ggcgtggccc cgccacaca gccaccgccc cctcatcccg ccgccccaaa cgtgcccaat 540
ggtcgattgc tgagctggaa tcacagtgcc gctgcagctg ctgcggcggc ggagcccaa 600
gcggcagcca actccatgaa cactcgtcgc gcggcggagg gttcatcgat gaccgggatt 660
aagggtcaga acctgggctt catctgcgtg gtgtgcccgc acaccagctc gggaaagcac 720
tacggaatcc tagcctgcaa tggctgctcc ggattcttca aacgcagcgt gcggcggaaa 780
ctcattttatc gctgccaggc gggaaacggga cgctgtgtgg tggacaaagc tcatcggaat 840
caatgccagg cctgcaggct caagaagtgc cttcaaattg gaatgaacaa ggacgacgac 900
tccatagatg taaccâacga caacgaggag ccgcattgcg tcagcagatc ggattcgagt 960
ttcattatgc cgcagttcat gtcgcccâat ctgtacaccc atcaacacga aacagtttac 1020
gagacaagtg cccggtgctt cttcatggcc gtcaagtggg ccaagaacct gccagctttt 1080
gcaagacttt ctttcgggga tcaggtâatt ttgctggagg agtcctggtc ggagctgttc 1140
ctgctgaacg caatccaatg gtgcattccc ctggatccca ccggtcgcgc cctcttctcg 1200
gtggcggagc actgcaataa tctagagaac aatgccaatg gcgacacttg cataacaaag 1260
gaggagctgg cggcggatgt gcgaacgctc cagcagatct tctgcaaata caaggcgggtg 1320
ctggtggacc ccgctgaatt cgcgtgcctc aaggcgatag ttctcttccg gccggâaacg 1380
cgcggaacta aagatccggc gcagatagag aatcttcagg atcaggcgca ccacacaaag 1440
acgcagttca ccgccagat agccagattc ggacgactcc ttctcatgct gccgttgctg 1500
cgcatgatca gctccacâaa gattgagtcc atctattttc agcgcaactat tgggaacacg 1560
cccattgâaa aggtgctctg tgacatgtat aagaactag 1599

```

&lt;210&gt; 23

&lt;211&gt; 484

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 23

```

Met Ser Asp Gly Val Ser Ile Leu His Ile Lys Gln Glu Val Asp Thr
1           5           10           15
Pro Ser Ala Ser Cys Phe Ser Pro Ser Ser Lys Ser Thr Ala Thr Gln
20          25          30
Ser Gly Thr Asn Gly Leu Lys Ser Ser Pro Ser Val Ser Pro Glu Arg
35          40          45
Gln Leu Cys Ser Ser Thr Thr Ser Leu Ser Cys Asp Leu His Asn Val
50          55          60
Ser Leu Ser Asn Asp Gly Asp Ser Leu Lys Gly Ser Gly Thr Ser Gly
65          70          75          80
Gly Asn Gly Gly Gly Gly Gly Gly Gly Thr Ser Gly Gly Asn Ala Thr
85          90          95
Asn Ala Ser Ala Gly Ala Gly Ser Gly Ser Val Arg Asp Glu Leu Arg
100         105         110
Arg Leu Cys Leu Val Cys Gly Asp Val Ala Ser Gly Phe His Tyr Gly
115         120         125
Val Ala Ser Cys Glu Ala Cys Lys Ala Phe Phe Lys Arg Thr Ile Gln
130         135         140
Gly Asn Ile Glu Tyr Thr Cys Pro Ala Asn Asn Glu Cys Glu Ile Asn
145         150         155         160

```

Lys Arg Arg Arg Lys Ala Cys Gln Ala Cys Arg Phe Gln Lys Cys Leu  
 165 170 175  
 Leu Met Gly Met Leu Lys Glu Gly Val Arg Leu Asp Arg Val Arg Gly  
 180 185 190  
 Gly Arg Gln Lys Tyr Arg Arg Asn Pro Val Ser Asn Ser Tyr Gln Thr  
 195 200 205  
 Met Gln Leu Leu Tyr Gln Ser Asn Thr Thr Ser Leu Cys Asp Val Lys  
 210 215 220  
 Ile Leu Glu Val Leu Asn Ser Tyr Glu Pro Asp Ala Leu Ser Val Gln  
 225 230 235 240  
 Thr Pro Pro Pro Gln Val His Thr Thr Ser Ile Thr Asn Asp Glu Ala  
 245 250 255  
 Ser Ser Ser Ser Gly Ser Ile Lys Leu Glu Ser Ser Val Val Thr Pro  
 260 265 270  
 Asn Gly Thr Cys Ile Phe Gln Asn Asn Asn Asn Asn Asp Pro Asn Glu  
 275 280 285  
 Ile Leu Ser Val Leu Ser Asp Ile Tyr Asp Lys Glu Leu Val Ser Val  
 290 295 300  
 Ile Gly Trp Ala Lys Gln Ile Pro Gly Phe Ile Asp Leu Pro Leu Asn  
 305 310 315 320  
 Asp Gln Met Lys Leu Leu Gln Val Ser Trp Ala Glu Ile Leu Thr Leu  
 325 330 335  
 Gln Leu Thr Phe Arg Ser Leu Pro Phe Asn Gly Lys Leu Cys Phe Ala  
 340 345 350  
 Thr Asp Val Trp Met Asp Glu His Leu Ala Lys Glu Cys Gly Tyr Thr  
 355 360 365  
 Glu Phe Tyr Tyr His Cys Val Gln Ile Ala Gln Arg Met Glu Arg Ile  
 370 375 380  
 Ser Pro Arg Arg Glu Glu Tyr Tyr Leu Leu Lys Ala Leu Leu Leu Ala  
 385 390 395 400  
 Asn Cys Asp Ile Leu Leu Asp Asp Gln Ser Ser Leu Arg Ala Phe Arg  
 405 410 415  
 Asp Thr Ile Leu Asn Ser Leu Asn Asp Val Val Tyr Leu Leu Arg His  
 420 425 430  
 Ser Ser Ala Val Ser His Gln Gln Leu Leu Leu Leu Leu Pro Ser  
 435 440 445  
 Leu Arg Gln Ala Asp Asp Ile Leu Arg Arg Phe Trp Arg Gly Ile Ala  
 450 455 460  
 Arg Asp Glu Val Ile Thr Met Lys Lys Leu Phe Leu Glu Met Leu Glu  
 465 470 475 480  
 Pro Leu Ala Arg

&lt;210&gt; 24

&lt;211&gt; 2529

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 , synthetic construct

&lt;400&gt; 24

ccctgggtcag	gtctggttca	ccaaaaaaga	aaataaaatt	acattttcaat	ctttccaata	60
tgcaaatatc	tgacgaaaa	ccagcgagaa	cagcatgctc	acaataaaga	gccccaaaac	120
aatgtgactc	gtatccgcgc	agagtgacgt	ttcgtgcctt	gcccagagtgc	caaatccaaa	180
tcccaatcca	ggcgacaaaa	atcgatgcag	atgctgtctg	cattctcata	gaaagtgcaa	240
ctgaataacc	gatggtcgcc	aaaagccacg	atgtccagta	ataatgacca	gtgaataaac	300
aattatgact	cgagcatcga	aaaatgctga	ggaacgaata	cataagcaat	aacaagaagg	360
tgctcaactc	ggacccaaaac	aagtactaca	tgctaacggt	cgaggaggcc	gatatgtatt	420
gacgttggtta	cagtggagct	gattacacaa	aagatcctca	gaacgatttt	atccaaggca	480

```

cgaacatgtc cgacggcgtc agcatcttgc acatcaaaaca ggaggtggac actccatcgg 540
cgctctgctt tagtcccagc tccaagtcaa cgccacgca gagtggcaca aacggcctga 600
aatcctcgcc ctcggtttcg ccggaaggc agctctgcag ctcgacgacc tctctatcct 660
gcgatttgca caatgtatcc ttaagcaatg atggcgatag tctgaaagga agtggtagaa 720
gtggcggcaa tggcggagga ggaggtggtg gtacgagtgg tggaaatgcg accaatgcga 780
gtgccggagc tggatcggga tccgtcaggg acgagctccg ccgattgtgt ttggtttgtg 840
gcgatgtggc cagtggattc cactatggtg tggcgagttg tgaggcttgc aaagcgttct 900
ttaaacgcac catccaaggc aacatcgagt acacgtgtcc ggcaacaac gagtgtgaga 960
ttaacaagcg gagacgcaag gcctgccaa gctgtcgctt ccagaaatgt ctactaatgg 1020
gcatgctcaa ggagggtgtg cgcttgatc gagttcgtgg aggacggcag aagtaccgaa 1080
ggaatcctgt atcaaaactct taccagacta tgcagctgct ataccaatcc aacaccacct 1140
cgctgtgcga tgtcaagata ctggaggtgc tcaattcata tgagccggat gccttgagcg 1200
tccaaacgcc gccgccgcaa gtccacacga ctagcataac taatgatgag gcctcatcct 1260
cctcgggcag cataaaactg gagtccagcg ttgttacgcc caatgggact tgcattttcc 1320
aaaacaacaa caacaatgat cccaatgaga tactaagcgt ccttagtgat atttacgaca 1380
aggaattggt cagcgtcatt ggctgggcca agcagatacc tggctttata gatctgccac 1440
ttaacgacca gatgaagctt ctccaggtgt cgtgggcaga gatcctgacg ctccagctga 1500
ccttcgggtc cctaccgttc aatggcaagt tatgcttcgc cacggatgtc tggatggatg 1560
aacatttggc caaggagtgc ggttacacgg agttctacta ccactgcgtc cagatcgcac 1620
agcgcatgga aagaatatcg ccacgaaggg aggagtacta cttgctaaag gcgctcctgc 1680
tggccaactg cgacattctg ctggatgatc agagtccct gcgcgcatct cgtgatacga 1740
ttcttaattc tctaaacgat gtggtctact tgctgcgtca ttcgtcggcc gtgtcgcac 1800
agcaacaatt gctgcttttg ctgccttcgc tgcggcaggc ggatgatata ctgcgaagat 1860
tttggcgtgg aattgcacgc gatgaagtca ttacatgaa gaaactgttc ctcgagatgc 1920
tcgagccgct ggccaggtga aaaggattat gcggcgccc aaactagttg atctagctga 1980
taagcaaagg tgcaaatata gtcttaggta tatatggatg tatactagag tagattaagc 2040
gtaggataag ccatgtatat aaatagtaaa atacttgtcg ggtaagatta gttcgcagaa 2100
aaaatctctt ttaatggact accaactaca gcaactggaa aaccctactt atcttctaga 2160
atcgggggtg gttacactg gttaaaggcg catatagggtg ttatgtgtct aaagttgtga 2220
gtcacagatc ttcaataatt tgttcaattc tcaactgggtc tgatatatgt atatgccgca 2280
accttctgat gtaacgtatg aatttgtggg cactttttaa atacgatag gggtctacaa 2340
tacaatggat tatactgttt ctaagtgtca tgaacccag tgattctgtg tctatgtggt 2400
acacatgcgg tcaaaagaat agcaatgtcg tccgtgaata ataaaccgtt tgtaactgtt 2460
gtttccatcc tccctaagtt ctgtattctt tggggatttt cttttcctaa acaaattcaa 2520
attagtttt 2529

```

&lt;210&gt; 25

&lt;211&gt; 601

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 25

```

Met Asp Gly Val Lys Val Glu Thr Phe Ile Lys Ser Glu Glu Asn Arg
1           5           10           15
Ala Met Pro Leu Ile Gly Gly Gly Ser Ala Ser Gly Gly Thr Pro Leu
20           25           30
Pro Gly Gly Gly Val Gly Met Gly Ala Gly Ala Ser Ala Thr Leu Ser
35           40           45
Val Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Arg His Tyr
50           55           60
Gly Ala Ile Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser Ile
65           70           75           80
Arg Lys Gln Leu Gly Tyr Gln Cys Arg Gly Ala Met Asn Cys Glu Val
85           90           95
Thr Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Gln Lys Cys
100          105          110

```

Leu	Ala	Ser	Gly	Met	Arg	Ser	Asp	Ser	Val	Gln	His	Glu	Arg	Lys	Pro
	115						120					125			
Ile	Val	Asp	Arg	Lys	Glu	Gly	Ile	Ile	Ala	Ala	Ala	Gly	Ser	Ser	Ser
	130					135						140			
Thr	Ser	Gly	Gly	Gly	Asn	Gly	Ser	Ser	Thr	Tyr	Leu	Ser	Gly	Lys	Ser
	145				150					155					160
Gly	Tyr	Gln	Gln	Gly	Arg	Gly	Lys	Gly	His	Ser	Val	Lys	Ala	Glu	Ser
				165					170					175	
Ala	Ala	Thr	Pro	Pro	Val	His	Ser	Ala	Pro	Ala	Thr	Ala	Phe	Asn	Leu
			180					185					190		
Asn	Glu	Asn	Ile	Phe	Pro	Met	Gly	Leu	Asn	Phe	Ala	Glu	Leu	Thr	Gln
	195						200					205			
Thr	Leu	Met	Phe	Ala	Thr	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	His
	210					215					220				
Gln	Gln	Ser	Gly	Ser	Tyr	Ser	Pro	Asp	Ile	Pro	Lys	Ala	Asp	Pro	Glu
	225				230					235					240
Asp	Asp	Glu	Asp	Asp	Ser	Met	Asp	Asn	Ser	Ser	Thr	Leu	Cys	Leu	Gln
				245				250						255	
Leu	Leu	Ala	Asn	Ser	Ala	Ser	Asn	Asn	Ser	Gln	His	Leu	Asn	Phe	
			260				265					270			
Asn	Ala	Gly	Glu	Val	Pro	Thr	Ala	Leu	Pro	Thr	Thr	Ser	Thr	Met	Gly
		275					280					285			
Leu	Ile	Gln	Ser	Ser	Leu	Asp	Met	Arg	Val	Ile	His	Lys	Gly	Leu	Gln
	290					295					300				
Ile	Leu	Gln	Pro	Ile	Gln	Asn	Gln	Leu	Glu	Arg	Asn	Gly	Asn	Leu	Ser
	305				310					315					320
Val	Lys	Pro	Glu	Cys	Asp	Ser	Glu	Ala	Glu	Asp	Ser	Gly	Thr	Glu	Asp
				325					330					335	
Ala	Val	Asp	Ala	Glu	Leu	Glu	His	Met	Glu	Leu	Asp	Phe	Glu	Cys	Gly
			340					345					350		
Gly	Asn	Arg	Ser	Gly	Gly	Ser	Asp	Phe	Ala	Ile	Asn	Glu	Ala	Val	Phe
	355						360					365			
Glu	Gln	Asp	Leu	Leu	Thr	Asp	Val	Gln	Cys	Ala	Phe	His	Val	Gln	Pro
	370					375						380			
Pro	Thr	Leu	Val	His	Ser	Tyr	Leu	Asn	Ile	His	Tyr	Val	Cys	Glu	Thr
	385				390					395					400
Gly	Ser	Arg	Ile	Ile	Phe	Leu	Thr	Ile	His	Thr	Leu	Arg	Lys	Val	Pro
				405					410					415	
Val	Phe	Glu	Gln	Leu	Glu	Ala	His	Thr	Gln	Val	Lys	Leu	Leu	Arg	Gly
			420					425					430		
Val	Trp	Pro	Ala	Leu	Met	Ala	Ile	Ala	Leu	Ala	Gln	Cys	Gln	Gly	Gln
		435					440					445			
Leu	Ser	Val	Pro	Thr	Ile	Ile	Gly	Gln	Phe	Ile	Gln	Ser	Thr	Arg	Gln
	450					455					460				
Leu	Ala	Asp	Ile	Asp	Lys	Ile	Glu	Pro	Leu	Lys	Ile	Ser	Lys	Met	Ala
	465				470				475						480
Asn	Leu	Thr	Arg	Thr	Leu	His	Asp	Phe	Val	Gln	Glu	Leu	Gln	Ser	Leu
				485				490						495	
Asp	Val	Thr	Asp	Met	Glu	Phe	Gly	Leu	Leu	Arg	Leu	Ile	Leu	Leu	Phe
			500					505					510		
Asn	Pro	Thr	Leu	Leu	Gln	Gln	Arg	Lys	Glu	Arg	Ser	Leu	Arg	Gly	Tyr
		515					520					525			
Val	Arg	Arg	Val	Gln	Leu	Tyr	Ala	Leu	Ser	Ser	Leu	Arg	Arg	Gln	Gly
	530					535						540			
Gly	Ile	Gly	Gly	Gly	Glu	Glu	Arg	Phe	Asn	Val	Leu	Val	Ala	Arg	Leu
	545				550				555						560
Leu	Pro	Leu	Ser	Ser	Leu	Asp	Ala	Glu	Ala	Met	Glu	Glu	Leu	Phe	Phe
				565				570						575	
Ala	Asn	Leu	Val	Gly	Gln	Met	Gln	Met	Asp	Ala	Leu	Ile	Pro	Phe	Ile
			580					585					590		



Leu Met Thr Ser Asn Thr Ser Gly Leu  
595 600

<210> 26

<211> 2288

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 26

```
attggaacaa ggagatttta ttgcgttaga aaaggttcaa aataggcaca aagtgcctga      60
aaatatcgta actgaccgga agtaacataa ctttaaccaa gtgcctcgaa aaatagatgt      120
ttttaaaagc tcaagaatgg tgataacaga cgtccaataa gaattttcaa agagccaaat      180
gtttgggttt cagttattta tacagccgac gactattttt tagccgcctg ctgtggcgac      240
aatggacggc gtttaaggttg agacgttcat caaaagcgaa gaaaaccgag cgatgccctt      300
gatcggagga ggcagtgcct caggcggcac tcctctgccca ggaggcggcg tgggaatggg      360
agccggagca tccgcaacgt tgagcgtgga gctgtgtttg gtgtgcgggg accgcgcctc      420
cgggcccggc tacggagcca taagctgcga aggctgcaag ggattcttca agcgctcgat      480
ccggaagcag ctgggctacc agtgctgcgg ggctatgaac tgcgagggtca ccaagcacca      540
caggaatcgg tgccagttct gtcgactaca gaagtgcctg gccagcggca tgcgaagtga      600
ttctgtgcag cagcagagga aaccgattgt ggacaggaag gaggggatca tcgctgctgc      660
cggtagctca tccactttctg gcggcggtaa tggctcgctc acctacctat ccggcaagtc      720
cggctatcag caggggcgtg gcaaggggca cagtgtaaag gccgaatccg cggccacgcc      780
tccagtgcac agcgcgccag caacggcctt caatttgaat gagaatatat tcccgatggg      840
tttgaatttc gcagaactaa cgcagacatt gatgttcgct acccaacagc agcagcaaca      900
acagcaacag catcaacaga gtggtagcta ttcgccagat attccgaagg cagatcccca      960
ggatgcagag gacgactcaa tggacaacag cagcacgctg tgcttgcaat tgctcgccaa     1020
cagcgccagc aacaacaact cgcagcactt gaactttaat gctgggggaa taccacccgc     1080
tctgcctacc acctcgacaa tggggcttat tcagagttcg ctggacatgc ggggtcatcca     1140
caagggaactg cagatcctgc agcccatcca aaaccaactg gagcgaatg gtaatctgag     1200
tgtgaagccc gagtgcgatt cagaggcggg ggacagtggc accgaggatg ccgtagacgc     1260
ggagctggag cacatggaac tagactttga gtgcggtggg aaccgaagcg gtggaagcga     1320
ttttgctatc aatgaggcgg tctttgaaca ggatcttctc accgatgtgc agtgtgcctt     1380
tcatgtgcaa ccgcccactt tgggtccactc gtattttaat attcattatg tgtgtgagac     1440
gggctcgcca atcatttttc tcaccatcca tacccttcga aaggttccag ttttcgaaca     1500
attggaagcc catacacagg tgaaactcct gagaggagtg tggccagcat taatggctat     1560
agctttggcg cagtgtcagg gtcagctttc ggtgccacc attatcgggc agtttattca     1620
aagcactcgc cagctagcgg atatcgataa gatcgaaccg ttgaagatct cgaagatggc     1680
aaatctcacc aggaccctgc acgactttgt ccaggagctc cagtcactgg atgttactga     1740
tatggagttt ggccttgctg gtctgatctt gctcttcaat ccaacgctct tgcagcagcg     1800
caaggagcgg tcgttgcgag gctacgtccg cagagtccaa ctctacgctc tgtcaagttt     1860
gagaaggcag ggtggcatcg gcggcggcga ggagcgcttt aatgttctgg tggctcgctt     1920
tcttccgctc agcagcctgg acgcagaggc catggaggag ctgttcttcg ccaacttggg     1980
ggggcagatg cagatggatg ctcttattcc gttcatactg atgaccagca acaccagtgg     2040
actgtaggcg gaattgagaa gaacagggcg caagcagatt cgctagactg cccaaaagca     2100
agactgaaga tggaccaagt gcgggcaata catgtagcaa ctaggcaaat cccattaatt     2160
atatatttaa tatatacaat atatagttta ggatacaata ttctaacata aaaccatggg     2220
tttattgttg ttcacagata aatggaatc gatttcccaa taaaagcgaa tatgttttta     2280
aacagaat
```

<210> 27

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 27

```

Met Asp Asn Cys Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys
 1          5          10          15
Glu Glu Val Lys Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser
 20          25          30
Ser Phe Ser Pro Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met
 35          40          45
Ser Met Val His Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn
 50          55          60
Asn Ser Ala Gly Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly
 65          70          75          80
Gly Ser Ala Ala Ala Val Gln Gln Gln Tyr Pro Pro Asn His Pro
 85          90          95
Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser
100          105          110
Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe
115          120          125
Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg
130          135          140
Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg
145          150          155          160
Tyr Gln Lys Cys Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu
165          170          175
Glu Arg Gln Arg Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser
180          185          190
Gly Gly Gly Ser Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln
195          200          205
Gly Gly Gly Gly Gly Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn
210          215          220
Gly Ser Asp Asp Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile
225          230          235          240
Glu Arg Ile Ile Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp
245          250          255
Arg Ala Leu Thr Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro
260          265          270
Asp Tyr Lys Gly Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln
275          280          285
Leu Phe Gln Met Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln
290          295          300
Val Pro Leu Asp Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu
305          310          315          320
Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp
325          330          335
Gly Gly Ala Gly Gly Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe
340          345          350
Glu Arg Arg Ser Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln
355          360          365
Ser Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala
370          375          380
Ile Phe Asp Arg Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu
385          390          395          400
Asn Leu Asp Arg Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr
405          410          415
Asn Pro Asp Ile Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys
420          425          430
Arg Glu Lys Val Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His
435          440          445
Pro Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Leu Arg Leu Pro Ala
450          455          460

```

Leu Arg Ser Ile Ser Leu Lys Cys Gln Asp His Leu Phe Leu Phe Arg  
 465 470 475 480  
 Ile Thr Ser Asp Arg Pro Leu Glu Glu Leu Phe Leu Glu Gln Leu Glu  
 485 490 495  
 Ala Pro Pro Pro Pro Gly Leu Ala Met Lys Leu Glu  
 500 505

<210> 28

<211> 2488

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 28

aaaaatgtcg	acgcgaaaaa	aggtattttat	tcattagtc	gaaagtcttg	cattctttgt	60
ttgttggtaa	aaagcgcaat	tgtttgagg	cgagcgaata	aagtgcgctg	ctccatcggc	120
tcaagattat	gtaaatgcag	caacgacccc	accaacaacg	aaactgcaac	ctgctccact	180
tggcccaacg	gaccaatagc	ggacggacgg	acacgggtgg	gttggcaaaag	tgaaacccca	240
acagagaggg	gaaagcgagc	caagacacac	cacatacaca	cgaagagaac	gagcaagaag	300
aaaccggtag	gcggaggagg	cgctgcccc	agttcctcca	atatacccag	caccacatca	360
caagcccagg	atggacaact	gcgaccagga	cgccagcttt	cggctgagcc	acatcaagga	420
ggaggtcaag	ccggacatct	cgcagctgaa	cgacagcaac	aacagcagct	tttcgcccga	480
ggccgagagt	cccgtgccct	tcatgcaggg	catgtccatg	gtccacgtgc	tgcccggctc	540
caactccgcc	agctccaaca	acaacagcgc	tggagatgcc	caaattggcgc	aggcgcccaa	600
ttcggctgga	ggctctgccg	ccgctgcagt	ccagcagcag	tatccgccta	accatccgct	660
gagcggcagc	aagcacctct	gctctatttg	cggggatcgg	gccagtggca	agcactacgg	720
cgtgtacagc	tgtgagggct	gcaagggtct	ctttaaacgc	acagtgcgca	aggatctcac	780
atacgtctgc	agggagaacc	gcaactgcat	catagacaag	cggcagagga	accgctgcc	840
gtactgccgc	taccagaagt	gcctaacctg	cggcatgaag	cgcaagcgg	tccaggagga	900
gcgtcaacgc	ggcgcccgca	atgcggcggg	taggctcagc	gccagcggag	gcggcagtag	960
cggtccaggt	tcggtagggc	gatccagctc	tcaaggcggg	ggaggaggag	gcggcgtttc	1020
tggcggaatg	ggcagcggca	acggttctga	tgacttcatg	accaatagcg	tgtccaggga	1080
tttctcgatc	gagcgcacat	tagaggccga	gcagcgagcg	gagacccaat	gcggcgatcg	1140
tgcactgacg	ttcctgcgcg	ttggtcccta	ttccacagtc	cagccggact	acaagggtgc	1200
cgtgtcggcc	ctgtgccaat	tggtcaacaa	acagctcttc	cagatggctg	aatacgcgcg	1260
catgatgcgc	cactttgccc	aggtgccgct	ggacgaccag	gtgattctgc	tgaaagccgc	1320
ttggatcgag	ctgctcattg	cgaacgtggc	ctgggtgcagc	atcgtttcgc	tggtatgacgg	1380
cggtgccggc	ggcggggggc	gtggactagg	ccacgatggc	tcctttgagc	gacgatcacc	1440
gggccttcag	ccccagcagc	tgttcctcaa	ccagagcttc	tcgtaccatc	gcaacagtgc	1500
gatcaaagcc	ggtgtgtcag	ccatcttcga	ccgcatattg	tcggagctga	gtgtaaagat	1560
gaagcggctg	aatctcgacc	gacgcgagct	gtcctgtctg	aaggccatca	tactgtacaa	1620
cccgacatac	cgcgggatca	agagccgggc	ggagatcgag	atgtgccgcg	agaagggtga	1680
cgtttgcctg	gacgagcact	gccgcctgga	acatccgggc	gacgatggac	gctttgcgca	1740
actgctgctg	cgtctgcocg	ctttgcgac	gatcagcctg	aagtgccagg	atcacctgtt	1800
cctcttcgcg	attaccagcg	accggccgct	ggaggagctc	tttctcgagc	agctggaggc	1860
gccgcgcgca	cccggccttg	cgatgaaact	ggagttaggt	cccgactcta	aagtctcccc	1920
cgtttctccat	ccgaaaaatg	tttcattgtg	attgcgtttg	tttgcatctt	tcctctctat	1980
cccttatacc	ctacaaaagc	cccctaatat	tacgcaaaat	gtgtatgtaa	ttgtttatatt	2040
tttttttatt	acctaataatt	attattatta	ttgatataga	aaatgttttc	cttaagatga	2100
agattagcct	cctcgacgtt	tatgtcccag	taaacgaaaa	acaaacaaaa	tccaaaactt	2160
gaaaagaaca	caaaacacga	acgagaaaaat	gcacacaagc	aaagtataag	taaaagttaa	2220
actaaagcta	aacgagtaaa	gatatttaaaa	taacgggttaa	aattaatgca	tagttatgat	2280
ctacagacgt	atgtaaacaat	acaaattcag	cataaatata	tatgtcagca	ggcgcatatc	2340
tgcgggtgctg	gccccgttct	aaatcaattg	ttaattacttt	ttaacataaaa	tttaccctaaa	2400
acgttatcaa	ttagatgcga	gatacaaaaa	tcaccgacga	aaaccaacaa	aatatatcta	2460
tgtataaaaa	atataaactg	cataacaa				2488

<210> 29  
 <211> 906  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 29  
 Met Gly Glu Glu Leu Pro Ile Leu Lys Gly Ile Leu Lys Gly Asn Val  
 1 5 10 15  
 Asn Tyr His Asn Ala Pro Val Arg Phe Gly Arg Val Pro Lys Arg Glu  
 20 25 30  
 Lys Ala Arg Ile Leu Ala Ala Met Gln Gln Ser Thr Gln Asn Arg Gly  
 35 40 45  
 Gln Gln Arg Ala Leu Ala Thr Glu Leu Asp Asp Gln Pro Arg Leu Leu  
 50 55 60  
 Ala Ala Val Leu Arg Ala His Leu Glu Thr Cys Glu Phe Thr Lys Glu  
 65 70 75 80  
 Lys Val Ser Ala Met Arg Gln Arg Ala Arg Asp Cys Pro Ser Tyr Ser  
 85 90 95  
 Met Pro Thr Leu Leu Ala Cys Pro Leu Asn Pro Ala Pro Glu Leu Gln  
 100 105 110  
 Ser Glu Gln Glu Phe Ser Gln Arg Phe Ala His Val Ile Arg Gly Val  
 115 120 125  
 Ile Asp Phe Ala Gly Met Ile Pro Gly Phe Gln Leu Leu Thr Gln Asp  
 130 135 140  
 Asp Lys Phe Thr Leu Leu Lys Ala Gly Leu Phe Asp Ala Leu Phe Val  
 145 150 155 160  
 Arg Leu Ile Cys Met Phe Asp Ser Ser Ile Asn Ser Ile Ile Cys Leu  
 165 170 175  
 Asn Gly Gln Val Met Arg Arg Asp Ala Ile Gln Asn Gly Ala Asn Ala  
 180 185 190  
 Arg Phe Leu Val Asp Ser Thr Phe Asn Phe Ala Glu Arg Met Asn Ser  
 195 200 205  
 Met Asn Leu Thr Asp Ala Glu Ile Gly Leu Phe Cys Ala Ile Val Leu  
 210 215 220  
 Ile Thr Pro Asp Arg Pro Gly Leu Arg Asn Leu Glu Leu Ile Glu Lys  
 225 230 235 240  
 Met Tyr Ser Arg Leu Lys Gly Cys Leu Gln Tyr Ile Val Ala Gln Asn  
 245 250 255  
 Arg Pro Asp Gln Pro Glu Phe Leu Ala Lys Leu Leu Glu Thr Met Pro  
 260 265 270  
 Asp Leu Arg Thr Leu Ser Thr Leu His Thr Glu Lys Leu Val Val Phe  
 275 280 285  
 Arg Thr Glu His Lys Glu Leu Leu Arg Gln Gln Met Trp Ser Met Glu  
 290 295 300  
 Asp Gly Asn Asn Ser Asp Gly Gln Gln Asn Lys Ser Pro Ser Gly Ser  
 305 310 315 320  
 Trp Ala Asp Ala Met Asp Val Glu Ala Ala Lys Ser Pro Leu Gly Ser  
 325 330 335  
 Val Ser Ser Thr Glu Ser Ala Asp Leu Asp Tyr Gly Ser Pro Ser Ser  
 340 345 350  
 Ser Gln Pro Gln Gly Val Ser Leu Pro Ser Pro Pro Gln Gln Gln Pro  
 355 360 365  
 Ser Ala Leu Ala Ser Ser Ala Pro Leu Leu Ala Ala Thr Leu Ser Gly  
 370 375 380  
 Gly Cys Pro Leu Arg Asn Arg Ala Asn Ser Gly Ser Ser Gly Asp Ser  
 385 390 395 400

Gly	Ala	Ala	Glu	Met	Asp	Ile	Val	Gly	Ser	His	Ala	His	Leu	Thr	Gln		
				405					410						415		
Asn	Gly	Leu	Thr	Ile	Thr	Pro	Ile	Val	Arg	His	Gln	Gln	Gln	Gln	Gln		
			420					425						430			
Gln	Gln	Gln	Gln	Ile	Gly	Ile	Leu	Asn	Asn	Ala	His	Ser	Arg	Asn	Leu		
		435					440						445				
Asn	Gly	Gly	His	Ala	Met	Cys	Gln	Gln	Gln	Gln	Gln	His	Pro	Gln	Leu		
	450					455						460					
His	His	His	Leu	Thr	Ala	Gly	Ala	Ala	Arg	Tyr	Arg	Lys	Leu	Asp	Ser		
465					470				475						480		
Pro	Thr	Asp	Ser	Gly	Ile	Glu	Ser	Gly	Asn	Glu	Lys	Asn	Glu	Cys	Lys		
				485					490						495		
Ala	Val	Ser	Ser	Gly	Gly	Ser	Ser	Ser	Cys	Ser	Ser	Pro	Arg	Ser	Ser		
			500					505					510				
Val	Asp	Asp	Ala	Leu	Asp	Cys	Ser	Asp	Ala	Ala	Ala	Asn	His	Asn	Gln		
	515						520					525					
Val	Val	Gln	His	Pro	Gln	Leu	Ser	Val	Val	Ser	Val	Ser	Pro	Val	Arg		
	530					535						540					
Ser	Pro	Gln	Pro	Ser	Thr	Ser	Ser	His	Leu	Lys	Arg	Gln	Ile	Val	Glu		
545					550				555						560		
Asp	Met	Pro	Val	Leu	Lys	Arg	Val	Leu	Gln	Ala	Pro	Pro	Leu	Tyr	Asp		
				565					570						575		
Thr	Asn	Ser	Leu	Met	Asp	Glu	Ala	Tyr	Lys	Pro	His	Lys	Lys	Phe	Arg		
			580					585						590			
Ala	Leu	Arg	His	Arg	Glu	Phe	Glu	Thr	Ala	Glu	Ala	Asp	Ala	Ser	Ser		
	595						600					605					
Ser	Thr	Ser	Gly	Ser	Asn	Ser	Leu	Ser	Ala	Gly	Ser	Pro	Arg	Gln	Ser		
	610				615						620						
Pro	Val	Pro	Asn	Ser	Val	Ala	Thr	Pro	Pro	Pro	Ser	Ala	Ala	Ser	Ala		
625					630					635					640		
Ala	Ala	Gly	Asn	Pro	Ala	Gln	Ser	Gln	Leu	His	Met	His	Leu	Thr	Arg		
			645					650						655			
Ser	Ser	Pro	Lys	Ala	Ser	Met	Ala	Ser	Ser	His	Ser	Val	Leu	Ala	Lys		
			660					665					670				
Ser	Leu	Met	Ala	Glu	Pro	Arg	Met	Thr	Pro	Glu	Gln	Met	Lys	Arg	Ser		
	675						680					685					
Asp	Ile	Gln	Asn	Tyr	Leu	Lys	Arg	Glu	Asn	Ser	Ser	Thr	Ala	Ala	Ser		
	690				695					700							
Ser	Thr	Thr	Asn	Gly	Val	Gly	Asn	Arg	Ser	Pro	Ser	Ser	Ser	Ser	Thr		
705					710				715						720		
Pro	Pro	Pro	Ser	Ala	Val	Gln	Asn	Gln	Gln	Arg	Trp	Gly	Ser	Ser	Ser		
				725					730						735		
Val	Ile	Thr	Thr	Thr	Cys	Gln	Gln	Arg	Gln	Gln	Ser	Val	Ser	Pro	His		
			740					745						750			
Ser	Asn	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser		
	755						760					765					
Ser	Ser	Ser	Ser	Thr	Ser	Ser	Asn	Cys	Ser	Ser	Ser	Ser	Ala	Ser	Ser		
	770					775						780					
Cys	Gln	Tyr	Phe	Gln	Ser	Pro	His	Ser	Thr	Ser	Asn	Gly	Thr	Ser	Ala		
785					790				795						800		
Pro	Ala	Ser	Ser	Ser	Ser	Gly	Ser	Asn	Ser	Ala	Thr	Pro	Leu	Leu	Glu		
				805				810						815			
Leu	Gln	Val	Asp	Ile	Ala	Asp	Ser	Ala	Gln	Pro	Leu	Asn	Leu	Ser	Lys		
			820					825					830				
Lys	Ser	Pro	Thr	Pro	Pro	Pro	Ser	Lys	Leu	His	Ala	Leu	Val	Ala	Ala		
		835					840					845					
Ala	Asn	Ala	Val	Gln	Arg	Tyr	Pro	Thr	Leu	Ser	Ala	Asp	Val	Thr	Val		
	850				855						860						
Thr	Ala	Ser	Asn	Gly	Gly	Pro	Pro	Ser	Ala	Ala	Ala	Ser	Pro	Ala	Pro		
865					870				875						880		

Ser Ser Ser Pro Pro Ala Ser Val Gly Ser Pro Asn Pro Gly Leu Ser  
 885 890 895  
 Ala Ala Val His Lys Val Met Leu Glu Ala  
 900 905

&lt;210&gt; 30

&lt;211&gt; 3750

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 30

```

agtcaaccgtc gcagtcgcag cagttgaggt tcgctctcct cgatttcggg caaatccgat      60
accatatagc acagcgtacc gcactctggg tatattcgta acgcgctttg gcttttacag      120
ttagtcgcgt tcgagacctt gtogagtttt gtcatgttag ccagcgatcc gcgggatccg      180
aaataagcca agaatcacaa cgcgagtgcg gcagttgcca gcagtaacta caccaatatt      240
tatattaatt aaaataaatt aaatgaaaca acatgctgat taatgccaat gaatgtttaa      300
tgcaattggt aatgtgaaga aaagtcgacc aagtctcccc aaaacaacac ttattcaaca      360
tccactacac actcgctttt ctggattacg cgcccaaaaa aaaacaaaaa ttaaaaatta      420
aaccaaaacca acaactaatt tatttgctaa atattccaaa aattcaatca atgtgaaaag      480
caagcaaaca aagttcctct cacaacaaaa cagcagttaa ttaaaatatt taaccgagat      540
aaagtgcaaa gaagataaca agttttctca gcaaacatcc atatgtacct gagtaccaac      600
caaaaagctg tgtgtgtgcc aaaaaccgaa gaggaattat ccaaaaatat ttaatgagca      660
agctcaactg agtggttgat gtgcccccca agggaaaagt gaccaagtca agatattttg      720
tcaaatcgaa cacagaaaac acaaaaatgg gcgaagaact cccgatattg aagggcatac      780
ttaaaggcaa cgtcaactat cacaatgcgc ctgtgcgttt tggacgcgtg ccgaagcgcg      840
aaaaggcgcg tatcctggcg gccatgcaac agagcaccga gaatcgcgcg cagcagcgag      900
ccctcgccac cgagctggat gaccagccac gcctcctcgc cgccgtgctg cgcgcccacc      960
tcgagacctg tgagttcacc aaggagaagg tctcgcgat gcggcagcg gcgcgggatt      1020
gccccctcta ctccatgccc acacttctgg cctgtccgct gaaccccgcc cctgaactgc      1080
aatcgagcaa ggagttctcg cagcgtttctg cccacgtaat tcgcggcgctg atcgactttg      1140
ccggcatgat tcccggtctc cagctgctca cccaggacga taagttcacg ctctgaagg      1200
cgggactctt cgacgcctcg tttgtgcgcc tgatctgcat gtttgactcg tcgataaaact      1260
caatcatctg tctaaatggc caggtgatgc gacgggatgc gatccagaac ggagccaatg      1320
cccgcttcct ggtggactcc accttcaatt tcgcggagcg catgaactcg atgaacctga      1380
cagatgccga gataggcctg ttctgcgcca cgttctgat tacgccgat cgccccggtt      1440
tgcgcaacct ggaggtgatc gagaagatgt actcgcgact caagggctgc ctgcagtaca      1500
ttgtcgccca gaataggccc gatcagcccg agttcctggc caagttgctg gagacgatgc      1560
ccgatctgcg caccctgagc accctgcaca ccgagaaaact ggtagttttc cgcaccgagc      1620
acaaggagct gctgcgccag cagatgtggt ccattggagga cggcaacaac agcgatggcc      1680
agcagaacaa gtcgccctcg ggcagctggg cggatgccat ggacgtggag gcggccaaga      1740
gtccgcttgg ctccgatcgc agcactgagt ccgccgacct ggactacggc agtccgagca      1800
gttcgcagcc acagggcgctg tctctgccct cgccgcctca gcaacagccc tcggctctgg      1860
ccagctcggc tctctgctg gcggccaccc tctccggagg atgtcccctg cgcaaccggg      1920
ccaattccgg ctccagcggt gactccggag cagctgagat ggatatcgtt ggctcgcacg      1980
cacatctcac ccagaacggg ctgacaatca cgccgattgt gcgacaccag cagcagcaac      2040
aacagcagca gcagatcgga atactcaata atgcgcattc ccgcaacttg aatgggggac      2100
acgcgatgtg ccagcaacag cagcagcacc cacaactgca ccaccacttg acagccggag      2160
ctgcccgccta cagaaaagcta gattcgccca cggattcggg cattgagtcg ggcaacgaga      2220
agaacgagtg caaggcggtg agttcggggg gaagttcctc gtgctccagt ccgcgttcca      2280
gtgtggatga tgcgctggac tgcagcgatg ccgccgccaa tcacaatcag gtggtgcagc      2340
atccgcagct gagtgtggtg tccgtgtcac cagttcgctc gcccagccc tccaccagca      2400
gccatctgaa gcgacagatt gtggaggata tgcccgtgct gaagcgctg ctgcaggctc      2460
ccccctgtga cgataccaac tcgctgatgg acgagcccta caagccgcac aagaaattcc      2520
gggcccctgc gcatcgcgag ttcgagaccg ccgaggcgga tgccagcagt tccacttccg      2580
gctcgaacag cctgagtgcc ggcagtccgc gacagagtcc agtcccgaac agtgtggcca      2640
cgcccccgcc atcggcggcc agcgcgcgcc caggtaatcc cgcccagagc cagctgcaca      2700
tgcacctgac ccgcagcagc cccaaggcct cgatggccag ctcgcactcg gtgctggcca      2760

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agtctctcat ggccgagccg cgcattgacgc ccgagcagat gaagcgcagc gatattatcc 2820
aaaactactt gaagcgcgag aacagcacag cagccagcag caccaccaat ggcgtgggca 2880
accgcagtcc cagcagcagc tccacaccgc cgccatcggc ggtccagaat cagcagcggt 2940
ggggcagcag ctccggtgatc accaccacct gccagcagcg ccagcagtec gtgtcgccgc 3000
acagcaacgg ttccagctcc agttcgagct ctactctccag ctccagttcg tcatcctcct 3060
ccacatcttc caactgcagc tccagctcgg ccagcagctg ccagtatttc cagtcgcccgc 3120
actccaccag caacggcacc agtgcaccgg cgagctccag ttcgggatcg aacagcgcca 3180
cgccccgtct ggaactgcag gtggacattg ctgactcggc gcagcctctc aatttggtcca 3240
agaaatcgcc cagcgcgccc cccagcaagc tgcacgctct ggtggccgcc gccaatgccg 3300
ttcaaaggta tcccacattg tccgcccagc tcacagtgc agcctccaat ggcggtcctc 3360
cgtcggcgcc ggccagtcgg gcgcccagca gcagtcggcc ggcgagtggt ggctccccc 3420
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caggaagcag gatcacttgg agcggcgggg gttgaattaa attattttac catttaattg 3600
agacgtgtac aaagtttgaa agcaaaaacca acatgcattg aatttaaaac taatatttaa 3660
agcaacaaca acaaaaacaa ctacaagtta ttaattttaa aaacaaacaa acaacaaac 3720
aacaacaaac ccaagcttga atggtattac 3750

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&lt;210&gt; 31

&lt;211&gt; 392

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 31

```

Met His Pro Ser His Leu Gln Gln Gln Gln Gln His Leu Leu Gln
1      5      10      15
Gln Gln Gln Gln Gln Gln His Gln Pro Gln Leu Gln Gln His His Gln
20     25     30
Leu Gln Gln Gln Pro His Val Ser Gly Val Arg Val Lys Thr Pro Ser
35     40     45
Thr Pro Gln Thr Pro Gln Met Cys Ser Ile Ala Ser Ser Pro Ser Glu
50     55     60
Leu Gly Gly Cys Asn Ser Ala Asn Asn Asn Asn Asn Asn Asn Asn
65     70     75     80
Ser Ser Ser Gly Asn Ala Ser Gly Gly Ser Gly Val Ser Val Gly Val
85     90     95
Val Val Val Gly Gly His Gln Gln Leu Val Gly Gly Ser Met Val Gly
100    105    110
Met Ala Gly Met Gly Thr Asp Ala His Gln Val Gly Met Cys His Asp
115    120    125
Gly Leu Ala Gly Thr Ala Asn Glu Leu Thr Val Tyr Asp Val Ile Met
130    135    140
Cys Val Ser Gln Ala His Arg Leu Asn Cys Ser Tyr Thr Glu Glu Leu
145    150    155    160
Thr Arg Glu Leu Met Arg Arg Pro Val Thr Val Pro Gln Asn Gly Ile
165    170    175
Ala Ser Thr Val Ala Glu Ser Leu Glu Phe Gln Lys Ile Trp Leu Trp
180    185    190
Gln Gln Phe Ser Ala Arg Val Thr Pro Gly Val Gln Arg Ile Val Glu
195    200    205
Phe Ala Lys Arg Val Pro Gly Phe Cys Asp Phe Thr Gln Asp Asp Gln
210    215    220
Leu Ile Leu Ile Lys Leu Gly Phe Phe Glu Val Trp Leu Thr His Val
225    230    235    240
Ala Arg Leu Ile Asn Glu Ala Thr Leu Thr Leu Asp Asp Gly Ala Tyr
245    250    255

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Leu Thr Arg Gln Gln Leu Glu Ile Leu Tyr Asp Ser Asp Phe Val Asn  
 260 265 270  
 Ala Leu Leu Asn Phe Ala Asn Thr Leu Asn Ala Tyr Gly Leu Ser Asp  
 275 280 285  
 Thr Glu Ile Gly Leu Phe Ser Ala Met Val Leu Leu Ala Ser Asp Arg  
 290 295 300  
 Ala Gly Leu Ser Glu Pro Lys Val Ile Gly Arg Ala Arg Glu Leu Val  
 305 310 315 320  
 Ala Glu Ala Leu Arg Val Gln Ile Leu Arg Ser Arg Ala Gly Ser Pro  
 325 330 335  
 Gln Ala Leu Gln Leu Met Pro Ala Leu Glu Ala Lys Ile Pro Glu Leu  
 340 345 350  
 Arg Ser Leu Gly Ala Lys His Phe Ser His Leu Asp Trp Leu Arg Met  
 355 360 365  
 Asn Trp Thr Lys Leu Arg Leu Pro Pro Leu Phe Ala Glu Ile Phe Asp  
 370 375 380  
 Ile Pro Lys Ala Asp Asp Glu Leu  
 385 390

&lt;210&gt; 32

&lt;211&gt; 3341

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 32

aagcattaac	gaaagaactg	cgcacaaagt	agggaggcaa	taattacata	tgtacatggc	60
tgggaaaggc	cttaactaaa	cttagcaaac	taataaatag	aaaaaaggaa	atattggcca	120
aattattatag	tattgggaat	attagggttac	ttgatatcaa	aaattaatgt	ctattttata	180
cacttattct	tagacttaat	gttaacttat	cgtacttatt	atgattgggt	tttcaagatt	240
accagaactt	gatagattgg	tctagctttt	gaaatcggat	agcattttct	ttaaaggact	300
ttgccatatg	ctaaagccta	acttcttttt	tcaattcagc	cacagctgac	aaaagcgaag	360
aaaatttgaa	agaccgtgaa	tcctttttgaa	acgccctctc	cggattcctc	attaagtgca	420
aaagatataa	catcgagag	atttcccata	aaaatgctga	tcaggcgccc	tcgcagggtg	480
ccaacgctga	tttccgccag	caggacgatg	atgaagatga	tgatgcccc	tctcaccgat	540
tcgatccgag	caacatggat	gtataccaaa	tagagctgga	ggaacaggca	caaattccgt	600
ccaaactgct	ggtcgaaacc	tgtgtgaagc	actcgtcttc	ggagcagcag	cagctccaag	660
ttaaagcagg	ggacctcatc	aaggatttca	ctcgggacga	ggaggaacag	ccaagcgaag	720
aggaggcgga	ggaagaggac	aacgaagagg	acgaggaaga	agaaggcgaa	gaagaagagg	780
aggacgagga	cgaggaagcc	ctgctgccgg	tagtcaattt	taatgcaaat	tcagacttta	840
atttgcattt	ctttgacaca	ccggaggact	cgtccaccca	aggggcctac	agtgaggcca	900
atagcttgga	atccgagcag	gaagaggaga	agcaaacaca	gcagcatcag	cagcagaagc	960
agcatcaccg	ggatttggag	gattgcctaa	gtgccattga	agctgatcca	ttgcagttgt	1020
tgcattgcga	cgacttctat	agaacatcag	ccctagcaga	gagtgttgca	gccagtctaa	1080
gcccacagca	gcagcagcaa	cggcagcaca	cccaccagca	acaacagcaa	cagcagcagc	1140
agcagcaaca	ccctggacag	cagcaacatc	agctcaactg	cacgctgagc	aatgggtggag	1200
gtgctttgta	caccatcagc	agtgtgcate	agttcgggtc	ggccagcaac	cacaacacca	1260
gcagcagctc	cccctcctcc	agcgcgcgcc	actcttcgcc	ggacagcggc	tgctcgtcgg	1320
cctcctcctc	cggtccttcg	cgatcctcgc	gatcctcctc	tgcatcctcc	tcctcgtcag	1380
cggtcagcag	caccatcagc	agcggccgca	gcagcaacaa	cagcgtcgtc	aaccccgag	1440
caacatcttc	atctgttgcg	catctgaaca	aagagcaaca	gcagcagcca	ctgccgacga	1500
cacagctgca	acagcagcag	cagcaccagc	agcagttgca	acacccgcag	cagcagcaat	1560
cttttggcct	agcagacagc	agcagcagca	acggcagcag	caacaacaac	aacggtgtct	1620
cctcgaaatc	atttgtgccc	tgcaaagtct	gtggcgacaa	ggcatcgagg	taccactatg	1680
gtgtaacctc	ctgcgaggg	tgcaagggat	tctttcgtcg	cagtatccag	aagcaaatcg	1740
aatacgcgtg	tttgcgggg	ggcaagtggc	tggtcatcag	actgaaccgc	aatcgctgcc	1800
agtactgccg	cttcaagaaa	tgcttttccg	ctggcatgag	ccgcgattcc	gtacgttatg	1860
gtcgcgttcc	caagcgttcc	cgtgagctga	acggagcggc	cgccctcctc	gccgccgctg	1920



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gagctcctgc ctccctcaat gtggatgact ctaccagcag cacactgcac ccgagtcacc 1980
tacagcagca gcagcaacag catctactac agcagcaaca gcagcagcaa catcagccac 2040
agctgcagca acaccaccaa ctgcaacagc agccgcgatgt aagcggcgta cgtgtgaaga 2100
ccccgagtac tccacaaacg ccacaaatgt gttcgatgcg ctctctcgcca tcggagctgg 2160
gcgggttgcaa tagtgccaat aacaataaca ataataacaa caacagtagc agcggtaatg 2220
ccagcgggtg cagcggcggtg agcgtcggcg ttgttgttgt gggcggacac cagcaactgg 2280
tgaggaggcag catggtggga atggcgggca tgggcacgga tgcccaccag gtgggcatgt 2340
gtcacgacgg cttggcggga acggcaaacg agctgaccgt ctacgatgtc atcatgtgcg 2400
tgtcgcaggc gcaccgcctc aactgctcct acacggagga actgaccaga gagctcatgc 2460
gtcgtcccgt gacggtgcc aaaaatggga ttgccagcac agtggccgag agtctggagt 2520
tccagaagat ctggctgtgg caacagttct cggccagggt gacgcctggc gttcagcgga 2580
ttgtggagtt tgcgaaacgc gtacctggct tctgtgattt caccacaagt gaccagctta 2640
tactaataaa gctgggcttc ttcgaggtct gggtgaccca tgtggcccg ttgatcaatg 2700
aggcgacatt gacactggac gatggtgcct acctgacgcg ccagcagctt gagatactct 2760
acgattctga ctttgtcaac gccttgctga actttgccaa cagctgaac gcctacgggc 2820
tgagtgcac cgaaatcgga ctcttctcgg ccattggtgct gcttgccctg gatcgagctg 2880
gactcagcga gcccaagggt atcggcaggg ccagggaact ggtggccgag gcgctgcgcg 2940
tacagatcct gcgttcgagg gcaggatccc caccggcgct gcagctgatg ccggcgctgg 3000
aagccaagat acccgagctg agatccttgg gggccaagca cttctcacac ctgactggc 3060
tacggatgaa ctggaccaag ctgcgcctgc cggccctctt cgccgagatc ttcgacatcc 3120
cgaaggctga cgatgagctg taggatgtgg agccaacccc gcgattccag ggccgtgcaa 3180
agcaaaccgc aacaagaaca gaatattcta ocactttagt gcttaagcaa cgtagctata 3240
gatcgaatg ggagggccgc agatcagata cagctctact cagcattacc ggagagatag 3300
tccactaagc ctatatgcat actactatac tagcagtgtt a 3341

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&lt;210&gt; 33

&lt;211&gt; 878

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 33

```

Met Lys Arg Arg Trp Ser Asn Asn Gly Gly Phe Met Arg Leu Pro Glu
1           5           10           15
Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Asn Gly Leu Val Leu Pro
20           25           30
Ser Gly Val Asn Met Ser Pro Ser Ser Leu Asp Ser His Asp Tyr Cys
35           40           45
Asp Gln Asp Leu Trp Leu Cys Gly Asn Glu Ser Gly Ser Phe Gly Gly
50           55           60
Ser Asn Gly His Gly Leu Ser Gln Gln Gln Gln Ser Val Ile Thr Leu
65           70           75           80
Ala Met His Gly Cys Ser Ser Thr Leu Pro Ala Gln Thr Thr Ile Ile
85           90           95
Pro Ile Asn Gly Asn Ala Asn Gly Asn Gly Gly Ser Thr Asn Gly Gln
100          105          110
Tyr Val Pro Gly Ala Thr Asn Leu Gly Ala Leu Ala Asn Gly Met Leu
115          120          125
Asn Gly Gly Phe Asn Gly Met Gln Gln Gln Ile Gln Asn Gly His Gly
130          135          140
Leu Ile Asn Ser Thr Thr Pro Ser Thr Pro Thr Pro Leu His Leu
145          150          155          160
Gln Gln Asn Leu Gly Gly Ala Gly Gly Gly Gly Ile Gly Gly Met Gly
165          170          175
Ile Leu His His Ala Asn Gly Thr Pro Asn Gly Leu Ile Gly Val Val
180          185          190
Gly Gly Gly Gly Gly Val Gly Leu Gly Val Gly Gly Gly Gly Val Gly
195          200          205

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Gly Leu Gly Met Gln His Thr Pro Arg Ser Asp Ser Val Asn Ser Ile  
 210 215 220  
 Ser Ser Gly Arg Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr  
 225 230 235 240  
 Ser Ala Asn Glu Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala  
 245 250 255  
 Pro Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser  
 260 265 270  
 Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe  
 275 280 285  
 Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg  
 290 295 300  
 Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg  
 305 310 315 320  
 Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro  
 325 330 335  
 Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu  
 340 345 350  
 Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly  
 355 360 365  
 Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu  
 370 375 380  
 Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu  
 385 390 395 400  
 Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu  
 405 410 415  
 Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp  
 420 425 430  
 Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln  
 435 440 445  
 Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr  
 450 455 460  
 Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly  
 465 470 475 480  
 Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu  
 485 490 495  
 Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr  
 500 505 510  
 Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr  
 515 520 525  
 Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu  
 530 535 540  
 Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu  
 545 550 555 560  
 Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu  
 565 570 575  
 Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr  
 580 585 590  
 Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu  
 595 600 605  
 Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu  
 610 615 620  
 Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg  
 625 630 635 640  
 Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro  
 645 650 655  
 Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg  
 660 665 670  
 Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr  
 675 680 685

Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala  
 690 695 700  
 Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu  
 705 710 715 720  
 Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln  
 725 730 735  
 Leu Pro Pro Gln Leu Gln Gly, Gln Leu Gln Pro Gln Leu Gln Pro Gln  
 740 745 750  
 Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu  
 755 760 765  
 Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu  
 770 775 780  
 Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile  
 785 790 795 800  
 Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr  
 805 810 815  
 Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val  
 820 825 830  
 Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr  
 835 840 845  
 Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu  
 850 855 860  
 Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr Ala  
 865 870 875

&lt;210&gt; 34

&lt;211&gt; 5586

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 34

tagtattttt	ttggactttg	ttgttaacgg	ttgttcgctc	gcacgtacga	agccccgatcg	60
cgttcgtcaa	aaaacaagat	acaaaataca	gcacacacaa	ttgaaaacga	caaccttaaca	120
gtacggtttc	ccaaagcacc	ttacatttca	aaaccgaaaa	cccccaaat	gttgtaacca	180
aataatgttt	aaatcacata	tacacctaca	tatatattatg	aaaaattggt	agacaaatcc	240
caaataatac	cagttccccc	aacaaccgca	acaaacacaa	gtgcaattca	tcggcaaaaa	300
ttaatataaa	gtgcaaatgc	attgtagctg	aaactcaaac	aatagtaaaa	atacatatcat	360
aagtgggtgaa	gaagcaaaag	gaaatagttc	ttaaaataac	gcaaatacgag	agcatatatatt	420
catatttgta	cagatattat	atggcggctg	catagtgcga	actgcggctg	aggggaatata	480
gcgggtatcga	aatgtaaata	ggaaacaacg	aagccagaac	tcgaaatcaa	acatcagcaa	540
cgtgacacac	agacataaga	cgcccgtcta	gtcgtggctc	gtggaacgct	agctccgctt	600
tgccaggagc	cggagacttt	ttccgcatcc	acaatattac	atatgtacat	atatcgaaga	660
tagtgcgcgga	gtgagtgagg	gatttgtgcc	gtggatcccg	atcccccttac	atatatatata	720
aggtagtgaa	aagattttac	tcaacattcc	aaatagtgc	ttgtcaactg	gaataccttt	780
tgttcaaata	cgcagtgggc	ccatggatac	ttgtggatta	gtagcagaac	tggcgacta	840
tatcgacgca	tatgctctga	ttgtttcccg	cactaaatga	gcagggattc	gggcgaaaaat	900
gtattttgaa	gcgaaacaag	tgcgcaaaaa	atactagctc	caccacgaaa	ctgcacaaaa	960
caccgcgaga	agcgagcaga	acctcggggc	gcacgaccga	gcttcgtaaa	gcaacagagg	1020
atcttaccag	gagatagctc	ttctccacat	agaccaactg	ccagggacaa	gctccttgtc	1080
cccagccgac	gctaagtga	cggaaaacgg	ccacaaaacg	gcgactatcg	gctgccagag	1140
gatgaagcgg	cgctggctga	acaacggcgg	cttcattgctc	ctaccggagg	agtcgtcctc	1200
ggaggtcacg	tcttcctcga	acgggctcgt	cctgccctcg	ggggtgaaca	tgctgccctc	1260
gtcgctggac	tcgcagcact	attgcatgca	ggacctttgg	ctctgcggca	acgagtcagg	1320
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ggccatgcac	gggtgctcca	gcactctgcc	cgcgagacaa	accatcattc	cgatcaacgg	1440
caacgcgaat	gggaatggag	gctccaccaa	tggccaatat	gtgcggggtg	ccactaatct	1500
gggagcggtg	gccaacggga	tgctcaatgg	gggcttcaat	ggaatgcagc	aacagattca	1560

gaatggccac	ggcctcatca	actccacaac	gccctcaacg	ccgaccaccc	cgctccacct	1620
tcagcagaac	ctggggggcg	cgggcgcg	cggtatcg	ggaatgggta	ttcttcacca	1680
cgcgaaatggc	accccaaatg	gccttatcgg	agttgtggga	ggcggcg	gagtaggtct	1740
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ggtgaattct	atatcttcag	gtcgcgatga	tctctcgcct	tcgagcagct	tgaacggata	1860
ctcggcgaac	gaaagctgcg	atgcgaagaa	gagcaagaag	ggacctgcgc	cacgggtgca	1920
agaggagctg	tgcttggttt	gcggcgacag	ggcctccggc	taccactaca	acgccctcac	1980
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caagtccggg	cgcgcctgcg	aaatggacat	gtacatgagg	cgaaagtgtc	aggagtgc	2100
cctgaaaaag	tgcttgccg	tgggtatgcg	gccggaatgc	gtcgtcccgg	agaaccaatg	2160
tgcgatgaag	cggcgcgaa	agaaggccca	ggaggagaag	gacaaaatga	ccacttcgcc	2220
gagctctcag	catggcgcca	atggcagctt	ggcctctggt	ggcggccaag	actttgttaa	2280
gaaggagatt	cttgacctta	tgacatgcga	gccgccccag	catgccacta	ttccgctact	2340
acctgatgaa	atattggcca	agtgtcaagc	gcgcaatata	ccttccttaa	cgtacaatca	2400
gttggccggt	atatacaagt	taatttggtg	ccaggatggc	tatgagcagc	catctgaaga	2460
ggatctcagg	cgtataatga	gtcaaccocga	tgagaacgag	agccaaacgg	acgtcagctt	2520
tcggcatata	accgagataa	ccatactcac	ggtcagbtg	attggttagt	ttgctaaagg	2580
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cattgaagac	ctgctgcatt	tctgcgcga	aatgttctcg	atgaagggtg	acaacgtcga	2820
atacgcgctt	ctcactgcc	ttgtgatott	ctcggaccgg	ccgggcctgg	agaaggccca	2880
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ggcggcagcc	gcgggccagc	atcagcctca	gcctcagccc	cagccccaac	cctcctccct	3300
gaccagaac	gattcccagc	accagagaca	cccgcagcta	caacctcagc	taccacctca	3360
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&lt;210&gt; 35

&lt;211&gt; 808

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 35

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20      25      30
Val Ala Asn Thr Thr Thr Thr Leu Gly Ser Ser Ala Gly Gly Ala Thr
35      40      45
Gly Ser Arg His Asn Val Ser Val Thr Asn Ile Lys Cys Glu Leu Asp
50      55      60
Glu Leu Pro Ser Pro Asn Gly Asn Met Val Pro Val Ile Ala Asn Tyr
65      70      75      80
Val His Gly Ser Leu Arg Ile Pro Leu Ser Gly His Ser Asn His Arg
85      90      95
Glu Ser Asp Ser Glu Glu Glu Leu Ala Ser Ile Glu Asn Leu Lys Val
100     105     110
Arg Arg Arg Thr Ala Ala Asp Lys Asn Gly Pro Arg Pro Met Ser Trp
115     120     125
Glu Gly Glu Leu Ser Asp Thr Glu Val Asn Gly Gly Glu Glu Leu Met
130     135     140
Glu Met Glu Pro Thr Ile Lys Ser Glu Val Val Pro Ala Val Ala Pro
145     150     155     160
Pro Gln Pro Val Cys Ala Leu Gln Pro Ile Lys Thr Glu Leu Glu Asn
165     170     175
Ile Ala Gly Glu Met Gln Ile Gln Glu Lys Cys Tyr Pro Gln Ser Asn
180     185     190
Thr Gln His His Ala Ala Thr Lys Leu Lys Val Ala Pro Thr Gln Ser
195     200     205
Asp Pro Ile Asn Leu Lys Phe Glu Pro Pro Leu Gly Asp Asn Ser Pro
210     215     220
Leu Leu Ala Ala Arg Ser Lys Ser Ser Ser Gly Gly His Leu Pro Leu
225     230     235     240
Pro Thr Asn Pro Ser Pro Asp Ser Ala Ile His Ser Val Tyr Thr His
245     250     255
Ser Ser Pro Ser Gln Ser Pro Leu Thr Ser Arg His Ala Pro Tyr Thr
260     265     270
Pro Ser Leu Ser Arg Asn Asn Ser Asp Ala Ser His Ser Ser Cys Tyr
275     280     285
Ser Tyr Ser Ser Glu Phe Ser Pro Thr His Ser Pro Ile Gln Ala Arg
290     295     300
His Ala Pro Pro Ala Gly Thr Leu Tyr Gly Asn His His Gly Ile Tyr
305     310     315     320

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Arg Gln Met Lys Val Glu Ala Ser Ser Thr Val Pro Ser Ser Gly Gln  
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 Glu Ala Gln Asn Leu Ser Met Asp Ser Ala Ser Ser Asn Leu Asp Thr  
 340 345 350  
 Val Gly Leu Gly Ser Ser His Pro Ala Ser Pro Ala Gly Ile Ser Arg  
 355 360 365  
 Gln Gln Leu Ile Asn Ser Pro Cys Pro Ile Cys Gly Asp Lys Ile Ser  
 370 375 380  
 Gly Phe His Tyr Gly Ile Phe Ser Cys Glu Ser Cys Lys Gly Phe Phe  
 385 390 395 400  
 Lys Arg Thr Val Gln Asn Arg Lys Asn Tyr Val Cys Val Arg Gly Gly  
 405 410 415  
 Pro Cys Gln Val Ser Ile Ser Thr Arg Lys Lys Cys Pro Ala Cys Arg  
 420 425 430  
 Phe Glu Lys Cys Leu Gln Lys Gly Met Lys Leu Glu Ala Ile Arg Glu  
 435 440 445  
 Asp Arg Thr Arg Gly Gly Arg Ser Thr Tyr Gln Cys Ser Tyr Thr Leu  
 450 455 460  
 Pro Asn Ser Met Leu Ser Pro Leu Leu Ser Pro Asp Gln Ala Ala Ala  
 465 470 475 480  
 Ala Ala Ala Ala Ala Ala Val Ala Ser Gln Gln Gln Pro His Gln Arg  
 485 490 495  
 Leu His Gln Leu Asn Gly Phe Gly Gly Val Pro Ile Pro Cys Ser Thr  
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 Ser Leu Pro Ala Ser Pro Ser Leu Ala Gly Thr Ser Val Lys Ser Glu  
 515 520 525  
 Glu Met Ala Glu Thr Gly Lys Gln Ser Leu Arg Thr Gly Ser Val Pro  
 530 535 540  
 Pro Leu Leu Gln Glu Ile Met Asp Val Glu His Leu Trp Gln Tyr Thr  
 545 550 555 560  
 Asp Ala Glu Leu Ala Arg Ile Asn Gln Pro Leu Ser Ala Phe Ala Ser  
 565 570 575  
 Gly Ser Ser Ser Ser Ser Ser Ser Ser Gly Thr Ser Ser Gly Ala His  
 580 585 590  
 Ala Gln Leu Thr Asn Pro Leu Leu Ala Ser Ala Gly Leu Ser Ser Asn  
 595 600 605  
 Gly Glu Asn Ala Asn Pro Asp Leu Ile Ala His Leu Cys Asn Val Ala  
 610 615 620  
 Asp His Arg Leu Tyr Lys Ile Val Lys Trp Cys Lys Ser Leu Pro Leu  
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 Phe Lys Asn Ile Ser Ile Asp Asp Gln Ile Cys Leu Leu Ile Asn Ser  
 645 650 655  
 Trp Cys Glu Leu Leu Phe Ser Cys Cys Phe Arg Ser Ile Asp Thr  
 660 665 670  
 Pro Gly Glu Ile Lys Met Ser Gln Gly Arg Lys Ile Thr Leu Ser Gln  
 675 680 685  
 Ala Lys Ser Asn Gly Leu Gln Thr Cys Ile Glu Arg Met Leu Asn Leu  
 690 695 700  
 Thr Asp His Leu Arg Arg Leu Arg Val Asp Arg Tyr Glu Tyr Val Ala  
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 Met Lys Val Ile Val Leu Leu Gln Ser Asp Thr Thr Glu Leu Gln Glu  
 725 730 735  
 Ala Val Lys Val Arg Glu Cys Gln Glu Lys Ala Leu Gln Ser Leu Gln  
 740 745 750  
 Ala Tyr Thr Leu Ala His Tyr Pro Asp Thr Pro Ser Lys Phe Gly Glu  
 755 760 765  
 Leu Leu Leu Arg Ile Pro Asp Leu Gln Arg Thr Cys Gln Leu Gly Lys  
 770 775 780  
 Glu Met Leu Thr Ile Lys Thr Arg Asp Gly Ala Asp Phe Asn Leu Leu  
 785 790 795 800

Met Glu Leu Leu Arg Gly Glu His  
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<210> 36

<211> 4841

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 36

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aagagtgg	ta	gcgcctacag	tggcatatgt	agttaaatcc	gtgaataagt	gaaaaatccg		180
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tgcaaca	gaa	atgtttatgc	cataatgtgc	acgcaaat	ta	ctatgaaaat		300
gtgactaga	aa	tgtgagtcga	acaaaacgag	taaaacgtga	aatcccaact	ggcttttggg		360
taacaaat	ct	tatcaacaca	gcaacggaaa	tacattaaaa	tcttgataga	ctgagaaagg		420
gacaattg	ga	atacttttag	ttatttttta	atgttttaca	acacaatgga	actgcatcaa		480
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&lt;210&gt; 37

&lt;211&gt; 7555

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 37

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&lt;210&gt; 38

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 38

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aagcaacaca	atctataaga	cgataatgca	ataactaact	tggaagcgtg	ggttctgtgc	540
aaacc						545

&lt;210&gt; 39

&lt;211&gt; 1119

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 39

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cagcgtgacc	gctacacttg	ttagggtgat	ggttcttaac	acaacctatt	aatttcccct	120
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&lt;210&gt; 40

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 40

gagagatgtg	cttcgttaaa	gcacaaaccc	30
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&lt;210&gt; 41

&lt;211&gt; 44

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 41  
ggactagtag atctagagga ttctacaaat gtccagtgtc tccc 44

<210> 42  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 42  
ccattattat cgccataatc gtaaagg 27

<210> 43  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 43  
attaccctgt tatccctagc gggttacctt aatgcgatca tcgccc 46

<210> 44  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 44  
ggaaagcttt tcctgctgat caataatacc 30

<210> 45  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 45  
tgggcccatc acttgcttgt aaccgccgaa gaactgcgcg g 41

<210> 46  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 46  
cgctagggat aacagggttaa taacagtcca cggtattagc ctatagg

47

<210> 47  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 47  
cgattatggc gataataatg gccaaagaga acatgggcaa catacgc

47

<210> 48  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 48  
gaagcaagcc tctagaaaga tgaagc

26

<210> 49  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 49  
cgtgccgttc tccatcgata cagtcaactg tctttgacc

39

<210> 50  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 50  
gcctggatag tcgatcaaatt gcg

23

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 51  
atggagaacg gcacggatgc 20

<210> 52  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 52  
tacattctag agaccaacta caacgacgag cccagtctgg 40

<210> 53  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 53  
cattcatcgg gacattaatt atgaacttgt tcagacgctc c 41

<210> 54  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 54  
gggcatcaac tccggaatta aatgcccgcac acgcatcgg 39

<210> 55  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 55  
gtctcacgac gttttgaacc cagaaatcga gctcgcccg gg 42

<210> 56  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 56

cacgaattcc aaactgtctc acgacgtttt gaaccc

36

<210> 57

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 57

gagagctagc atgccggcta gatctcgaga tcggccggcc tagg

44

<210> 58

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 58

gaactgcagc tcgagagcta gcatgccggc

30

<210> 59

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 59

ggagatatatc atatggctag catgactggg gg

32

<210> 60

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 60

tgctcgaagc ttcgcagaag ataatagtag g

31